```
Query Match
Best Local Simi
Matches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-974-899-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-974-899-24
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
512.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -
    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Appli
Sequence 5, Appli
Sequence 50, Appl
                                                                                                                                                                                                                                                                               April 13, 2006, 17:19:00 ; Search time 35.4017 Seconds (without alignments) 282.578 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     649
1 BVQLVESGGGLVQPGGSLRL........FYGTTYFDYWGQGTLVTVSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
Sequence
Sequence
                                         GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cgm2_6/ptcdata/1/iaa/5_COMB.pep:*
/cgm2_6/ptcdata/1/iaa/6_COMB.pep:*
/cgm2_6/ptcdata/1/iaa/H_COMB.pep:*
/cgm2_6/ptcdata/1/iaa/PCTM2_COMB.pep:*
/cgm2_6/ptcdata/1/iaa/RB_COMB.pep:*
/cgm2_6/ptcdata/1/iaa/RB_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-804-444A-50

US-09-02-985-50

US-09-121-952A-50

US-09-234-340A-50

US-09-35-014-50

US-09-35-014-50

US-08-437-642B-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-146-206C-20
US-09-705-686-20
US-09-705-392A-20
US-09-705-398-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5-08-804-444A-52
5-08-804-444A-55
5-09-026-985-52
5-09-026-985-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                572060 seqs, 82675679 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                         - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Issued Patents AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-727-737-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   %
Query
Match Length D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5548.5
5548.5
5548.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
5550.5
55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Title:
Ferfect score:
                                                                                                                                                                                                             OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database
                                                                                                                                                                                                                                                                                        Run on:
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                       Gaps
                                                      Sequence
   Sequence
Sequence
Sequence
Sequence
                                                                           Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 24, Application US/08974899;
Patent No. 6037454;
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: PROBRESS:
CORRESPONDENCES: 24
CORRESPONDENCES.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 649; DB 2;
Similarity 100.0%; Pred. No. 7.7e-57;
21; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: WinPatin (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,899
US-09-355-014-55
US-09-355-014-55
US-09-027-912-70
US-09-121-952A-70
US-09-121-952A-70
US-09-027-449-60
US-09-027-449-60
US-09-121-952A-60
US-09-121-952A-60
US-09-121-952A-60
US-09-121-952A-60
US-09-121-952A-60
US-09-121-952A-60
US-09-121-952A-60
US-09-121-952A-71
US-09-026-985-71
US-09-027-449-71
US-09-027-449-71
US-09-027-449-71
US-09-027-449-71
                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 11/27/96
ATTONNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELEPHONE: 650/225-1994
TELEPHONE: 650/225-1998
TELEPHONE: 650/225-1998
TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FOPOLOGY: Linear
```

```
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                             61 NQKFKDRPTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 NQKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYPDYWGQGTLVTVS 120
61 NOKRYDRFIISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 NQKPKDRPTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 BVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMWWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 24, Application US/09795798

Patent No. 6703018

GENERAL INFORMATION:

TITLE OF INVENTION: Humanized Anti-CD11a Antibodies

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSE: Genentech, Inc.

STREET: 1 DAA Way

CITY: South San Prancisco

STATE: California

COUVTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 MD floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: NinPatin (Genentech)

COMPUTER: SETION DATA:

PELING DATE: 28-Peb-2001

CLASSIFICATION NAMBER: USUNGOND>

PUTOR ADPLICATION DATE:

CLASSIFICATION DATE:

CLASSIFICATION DATE:

COMPUTER: ADPLICATION DATE:

CLASSIFICATION DATE:

CLASSIFICATION DATE:

CLASSIFICATION DATE:

COMPUTER:

CLASSIFICATION DATE:

CLASSIFICATION DATE:

CLASSIFICATION DATE:

CLASSIFICATION DATE:

COMPUTER:

CLASSIFICATION DATE:

CLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 649; DB 2;
; Pred. No. 7.7e-57;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/974,899
FILING DATE: CURLOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERIŞTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 121 amino acida
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/08974899 Patent No. 6037454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%;
Matches 121; Conservative 0
                                                                                                                                                       121 $ 121
                                                                                                                                                                                                                                     121 S 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 $ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 $ 121
                                                                                                                                                                                                                                                                                                                                                                                             US-09-795-798-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-795-798-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-08-974-899-5
                                                                         셤
                                                                                                                                                       ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
```

```
61 NOKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 NQKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIHPSDSETRY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS: 4
CORRESPONDENCE ADDRESS: 4
CORRESPONDENCE ADDRESS: 6
CORREST: 1 DNA Way
CITY: South San Francisco
STARET: California
COUNTRY: USA
ZIP: 94080
COMPUTER: READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.055/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/09795798

Patent No. 6703018
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Presta, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 632; DB 2;
Pred. No. 3.7e-55;
1; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION 536
PRIOR PAPLICATION DATE:
APPLICATION NUMBER: 60/031971
FILING DATE: 11/27/96
ATTONNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET VUMBER: 91014R1
TELEPHONE: 650/225-1994
TELEPHONE: 650/522-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94080
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 121 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 96.7
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 8 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 S 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
US-09-795-798-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-974-899-5
```

```
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B. 6.59
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 91085R3-2
TELEPHONE: 650/225-5530
TELEPHONE: 650/225-5530
TELEPHONE SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 50, Application US/08804444A Patent No. 6117980 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Genentech, Inc. STREET: 1 DNA Way CITY: South San Francisco STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: Amino acide

TOPOLOGY: Linear
US-08-804-444A-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 103; Conservative
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                              ; TOPOLOGY: Linear
US-09-027-449-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
US-08-804-444A-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 NOKFKORFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 NOXPKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGGGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EVOLVESGGGLVQPGGSLRLSCAASGYSFTGHWMWWVRQAPGKGLEWVGMIHPSDSETRY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 BVQLVBSGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania R.
APPLICANT: Geneng, Steven R.
APPLICANT: Preets, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SUFUNES: 72
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DAR WAY
CITY: South San Francisco
STREET: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 97.4%; Score 632; DB 2; Length 121; Best Local Similarity 96.7%; Pred. No. 3.7e-55; Matches 117; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winterin Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,449
FILING DATE: 20-Peb-1998
                                      SOFTWARE: WIDEALLE CURRENT APPLICATION DATA:

PULLING DATE: 28-Feb-2001
CLASSIFICATION NUMBER: US/9/795,798
FILING DATE: 28-Feb-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: cUnknown>
PILING DATE: cunknown>
ATTORNEY/AGENT INPORMATION:
NAMME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REPERENCE/DOCKET NUMBER: P1014R1
TELEPHONE: 650/25-1994
TELEPHONE: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
FUNCTH: 121 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-027-449-50
Sequence 50, Application US/09027449
Patent No. 6025158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074,330
FILING DATE: 22-Jan-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 121 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 S 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-795-798-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   뎚
```

```
1;
                                    ï
                                                                                                   1 EVOLVESGGGLVQPGGSLRLSCAASGFSFTGHWMNWVRQAPGKGLEWVGMIHPSDSETRY 60
                                                                                                                                      61 NQKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYC-ARGIYFYGTTYFDYWGQGT 115
                                                                                                                                                                       61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAARGIYFYGTTYFDYWGQGT 116
                                    1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                     APPLICANT: Gonzalez, Tania N
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
ATTLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 116;
   DB 2; Length 116;
Query Match
84.5%; Score 548.5; DB 2; Length 1
Best Local Similarity 88.8%; Pred. No. 6.2e-47;
Matches 103; Conservative 2; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84.5%; Score 548.5; DB 2;
88.8%; Pred. No. 6.2e-47;
iive 2; Mismatches 10;
```

```
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                1 EVQLVESGGGLVQPGGSLRLSCAASGPSFTGHWANAWVRQAPGKGLEWVGMIHPSDSETRY 60
1 BVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EVQLVESGGGLVQPGGSLRLSCAASGFSFTGHWMWWVRQAPGKGLEWVGMIHPSDSETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAARGIYFYGTTYFDYWGGGT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 NQKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYC-ARGIYFYGTTYFDYWGQGT 115
                                                                                                         61 NOKFKDRFTISVDKSKNTLYLOMNSLRAEDTAVYYC-ARGIYFYGTTYFDYWGOGT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAARGIYFYGTTYFDYWGQGT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gonzalez, Tania R.
APPLICANT: Brong, Steven R.
APPLICANT: Prests. Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
CORRESPONDENCES. 72
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84.5%; Score 548.5; DB 2; Length 116; 88.8%; Pred. No. 6.2e-47; ive 2; Mismatches 10; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: PC-DOS/MS-DOS SOFTWARE: Winbatin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/026,985 FILING DATE: 20-Feb-1998 CLASSIFICATION: ATTORNEY/AGENT INFORMATION: ATTORNEY/AGENT INFORMATION: REFERENCE/DOCKET NUMBER: 34,659 REFERENCE/DOCKET NUMBER: 91085R3-1 TELECHMUNICATION INFORMATION: TELECHMUNICATION SOFTENCE/DOCKET NUMBER: 10185R3-1 TELECHMUNICATION SOFTENCE/DOCKET NUMBER: 550/225-5530 TELERPAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 50: CTOMING CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 50, Application US/09121952A
Patent No. 6458355
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Heei, Vanessa
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shahrokh, Zahra
                                                                                                                                                                                                                                                                                                     Sequence 50, Application US/09026985
Patent No. 6133426
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 88.8 Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-121-952A-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-026-985-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                         ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
```

```
| TITLE OF INVENTION: METHODS OF TREATING INFLAMENT-POLYMER CONJUGATES
| MUMBER OF ENCURATION: METHODS OF TREATING INFLAMENT-POLYMER CONJUGATES
| MUMBER OF SEQUENCES: 12
| ADDRESSER: Generate Aldress: 13
| ADDRESSER: Generate CALL SAR | Transcription | T
```

1; Gaps

```
1 EVQLVESGGGLVQPGGSLRLSCAASGFSFTGHWMWWVRQAPGKGLEWVGMIHPSDSETRY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ADSVKGRFIISRDNSKNTLYLQMNSLRAEDTAVYYCAARGIYFYGTTYFDYWGQGT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 NOKFKDRFTISVDKSKNTLYLOMNSLRAEDTAVYYC-ARGIYFYGTTYFDYWGQGT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

84.5%; Score 548.5; DB 2; Length 116;
Best Local Similarity 88.8%; Pred. No. 6.2e-47;
Matches 103; Conservative 2; Mismatches 10; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: 35. inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION: 530

PRION APPLICATION: 530

PRION APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: PCT/US92/05126

FILING DATE: 15-UND-1992

PRION APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: 07/715272

FILING DATE: 15-UND-1991

ATTORNEY/AGENT INFORMATION: NUMBER: Lee, Wendy M. NUMBER: DECEMBER DECEMBER: DECEMBER DECEMBER DECEMBER DECEMBER. DECEMBER DECEMBER DECEMBER. DECEMBER DECEM
FILING DATE: 21-Jul-1999
CLASSIFICATION: CURMOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFOMM 650/252-5530
TELEFORMS 650/252-5530
TELEFORMS 500 ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Deal J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; SEQUENCE DESCRIPTION: SEQ ID NO: 50: 108-09-355-014-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P0709P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-07-934-373C-20
; Sequence 20, Application US/07934373C
Patent No. 5821337
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: PO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 122 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EVQLVESGGGLVQPGGSLRLSCAASGPSFTGHWMAWVRQAPGKGLEWVGMIHPSDSETRY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EVQLVESGGGLVQPGGSLRLSCAASGYSPTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 NOKPKDRPTISVDKSKNTLYLQMNSLRAEDTAVYYC-ARGIYFYGTTYFDYWGQGT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAARGIYFYGTTYFDYWGQGT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 1, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S-09-155-014-55
Sequence 50, Application US/09355014
Sequence 60, Application US/09355014
Patent No. 687003
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Hsei, Vanessa
Leong, Steven R.
Presta, Leonard G.
Shahrokh, Zahra
Shahrokh, Zahra
TILE OF INVENTION: Antibody Fragment-Polymer Conjugates and
Humanized Anti-IL-8 Monoclonal Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIF: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinDatin (Genentech)
CURRYT APPLICATION DATA:
APPLICATION NUMBER: US/09/355,014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 84.5%; Score 548.5; DB 2; Best Local Similarity 88.8%; Pred. No. 6.2e-47; Matches 103; Conservative 2; Mismatches 10;
                                                                         MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-LUCS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,340A
FILING DATE:
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/121,952
FILING DATE: 24-Jul-1998
APPLICATION NUMBER: 60/07430
FILING DATE: 22-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/075467
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 9108584
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
TENACH 116 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 116 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: Linear
US-09-234-340A-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
US-09-355-014-50
```

The said to the said

```
61 NQKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTT--YFDYWGQGTLVT 118
                                                                                                                                     61 NOKEKDRFTISVDKSKNTAYLQMNSLRAEDTAVYYCARSGY-YGDSDWYFDVWGQGTLVT 119
                         1 BVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY 60
                                                   1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGYTWNWVRQAPGKGLEWVALINPYKGVSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P0709P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40,378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 122 amino acids
Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 83.73
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94080
COMPUTER READABLE FORM:
                                                                                                                                                                                         119 VSS 121
                                                                                                                                                                                                                              120 VSS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 VSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 VSS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-146-206C-20
                                                                                                                                                                                                                                                                                                                    JS-08-146-206C-20
                                                            셤
                                                                                                     ሯ
                                                                                                                                     셤
                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ñ
                                                                                                                                                                                                                                  61 NQKFKDRFTISVDKSKNTAYLQMNSLRAEDTAVYYCARSGY-YGDSDWYFDVWGGGTLVT 119
                                                                                                                                                                   9
                                                                                                                                              1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGYTWNWRQAPGKGLEWVALINPYKGVSTY
                                                                                                                                                                                                          61 NOKFKDRFTISVDKSKNTLYLOMNSLRAEDTAVYYCARGIYFYGTT--YFDYWGQGTLVT
                                                                                                                        1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                      Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                    3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3,
                                           DB 1; Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 122;
                                    Query Match

80.24; Score 520.5; DB 1; Length
Best Local Similarity 83.74; Pred. No. 3.9e-44;
Matches 103; Conservative 4; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 520.5; DB 2;
Pred. No. 3.9e-44;
4; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20, Application US/08437642B
Patent No. 6054297
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Winderin (Genencech)
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
CLASSIFICATION: 530
RIGASPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
RIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
FILING DATE: 14-JUN-1993
APPLICATION NUMBER: 15-JUN-1993
FILING DATE: 14-JUN-1991
FILING DATE: 14-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P0709P2C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0705
TELEPHONE: 650/22-1994
TELEPHONE: 650/22-1994
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 83.7%;
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 122 amino acids
Amino Acid
                                                                                                                                                                                                                                                                                            119 VSS 121
                                                                                                                                                                                                                                                                                                                                     120 VSS 122
US-07-934-373C-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY:
US-08-437-642B-20
                                                                                                                                                                                                          ઠ
                                                                                                                                                                                                                                                                                        ò
```

```
61 NQKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTT--YFDYWGQGTLVT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 NQKFKDRFTISVDKSKNTAYLQMNSLRAEDTAVYYCARSGY-YGDSDWYFDVWGQGTLVT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGYTMNWVRQAPGKGLEWVALINPYKGVSTY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EVOLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
Sequence 20, Application US/08146206C

Patent No. 6407213

GENERAL INFORMATION:

APPLICANT: Carter, Paul J.

APPLICANT: Persta, Leonard G.

TITLE OF INVENTION: Method for Making Humanized Antibodies

TUMBER OF SEQUENCES: 26

CORRESPONDENCES:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 520.5; DB 2; Length 122;
Pred. No. 3.9e-44;
4; Mismatches 13; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 18M PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winderin (Genentech) CURRENT APPLICATION DATA: WS/08/146,206C FILING DATE: 17-No. 6407213-1993 CLASSIFICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: 0/715272 FILING DATE: 14-UTW-1991 ATTORNEY/AGENT INFORMATION:
```

us-10-727-737-17.rai

```
61 NOKPKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTT--YFDYWGQGTLVT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGYTWNWVRQAPGKGLEWVALINPYKGVSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EVOLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Gaps
                                                                                                                      Presta' Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies NUMBER OF SEQUENCES: 26
CORRESPONDENCE JESSES: ADDRESSE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20, Application US/09705392A
Patent No. 6719971
GENERAL INPORMATION:
APPLICANT: Carter, Paul J.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80.2%; Score 520.5; DB 2; Length 122; 83.7%; Pred. No. 3.9e-44; tive 4; Mismatches 13; Indels 3
                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,686
FILING DATE: 02-No. 6639055-2000
CLASSIPTCATION AURICANNON-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709FLD3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO: 20:
                                          Sequence 20, Application US/09705686 Patent No. 6639055 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 650/225-1994
TELEPAX: 650/552-9881
INFORWATION POR SEO. ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 122 amino acids TYPE: Amino Acid
                                                                                                          APPLICANT: Carter, Paul J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 83.7
Matches 103, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 VSS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 VSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-705-392A-20
RESULT 14
US-09-705-686-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JS-09-705-686-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
```

```
61 NOKFKORFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTT--YFDYWGQGTLVT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 NQKFKDRFTISVDKSKNTAYLQMNSLRAEDTAVYYCARSGY-YGDSDWYFDVWGQGTLVT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EVQLVBSGGGLVQPGGSLRLSCAASGYSFTGYTMNWVRQAPGKGLEWVALINPYKGVSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 520.5; DB 2; Length
Pred. No. 3.9e-44;
4; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNAY AGENT INFORMATION:

NAME: Lee, Wendy M.

REGISTRATION NUMBER: 40,378

REGISTRATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFRANCE, 620/225-1994

TELEFRAN: 650/952-9881

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTSTICS:

SEROTH: 122 amino acids

TYPE: Amino Acid
                                                                                                                      COMPUTER: 15. inch, 1.44 Mb floppy disk COMPUTER: 15. inch, 1.44 Mb floppy disk COMPUTER: 15. inch, 1.44 Mb floppy disk COMPUTER: 15M PC compatible OPERATING SUSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/705, 392A FILING DATE: 02-No. 6719971-2002

CLASSIFICATION: vUnknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/146206

FILING DATE: 17-NOV-1993

APPLICATION NUMBER: 07/715272

FILING DATE: 14-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-705-392A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: April 13, 2006, 17:20:46 Job time : 36.4017 secs
CITY: South San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 80.2%;
Best Local Similarity 83.7%;
Matches 103; Conservative 4
                                                                             ZIP: 94080
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 VSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 VSS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

## THIS PAGE IS BLANK

```
ALIGNMENTS
                                            AEB27726
AEB17636
ADS33304
ADW03410
                                                                                                                                 ADW03411
AEB27728
ABB27728
ADP79584
ADW03309
ADW03109
ADW21312
ADW21320
ADW221320
ADW229444
AAY29444
AAY29444
  516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1
    April 13, 2006, 17:05:24 ; Search time 246.227 Seconds (without alignments) 215.918 Million cell updates/sec
                                                                                                                                                                                                                                                                                      1 EVQLVESGGGLVQPGGSLRL.....FYGTTYFDYWGQGTLVTVSS 121
                    GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   2443163
                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                     2443163 segs, 439378781 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          length: 0
length: 2000000000
                                                                                                                                                                                                                                            US-10-727-737-17
```

Perfect score:

Title:

Eun on:

Sequence:

Scoring table:

Searched:

Heavy cha 2H7.v16 H 2H7.v31 L

ant ant ant

Human Mouse Human

Aeb27726 Aeb17636 Aeb17636 Aew03410 Aew03411 Aew03411 Aeb17638 Aeb17638 Aeb17638 Aeb17638 Aeb1339 Aew03406 Aew03464 Aew0346 Ae

Humanized Variable Anti-CD20

Humanized Humanized Humanized Mouse ant Humanized Humanized Humanised Humanised Humanised

geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\* geneseqp2005s:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\* Geneseq 21:\* ...........

seq

Minimum DB Maximum DB M

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

The present sequence represents the heavy chain of a "rhesusised" (sic) humanised anti-CD11a antibody that binds specifically to the human CD11a I domain (MHM24 epitope). CD11a refers to the alpha subunit of lymphocyte function-associated antigen I (LFA-1) from any mammal. The humanised anti-CD11a antibodies are used to determine presence of CD11a in usual amentosasys or by in vivo imaging, particularly for diagnosis of CD11a associated diseases (typically immune responses and inflammation such as peoriasis, Crohn's disease, rheumatoid arthritis, transplant rejection,

leukaemia, etc

New humanised anti-CD11a antibody - used in immunoassays for CD11a, and also to treat conditions such as immunological or inflammatory disease. Complementarity determining region; heavy chain variable region; humanised antibody; MRM24F(ab)-8; anti-CD11a antibody; human CD11a I domain; MFM24 epitope; alpha subunit; lymphocyte function-associated antigen 1; LFA-1; immunoassay; Rhesusised heavy chain of humanised anti-CD11a antibody in vivo imaging; diagnosis; CD11a-associated disease. AAW62019 standard; peptide; 121 AA Disclosure, Page 56, 66pp, English. 97WO-US019041. 96US-00757205. (first entry) Jardieu PM, Presta LG; (GETH ) GENENTECH INC. WPI; 1998-322737/28. WO9823761-A1. 01-OCT-1998 Unidentified 20-OCT-1997; 27-NOV-1996; 04-JUN-1998. AAW62019; AAW62019 

```
US6037454-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-MAR-2000
                                                                                                                                                                                                                                                                                                                                 AAY82348;
                                                                Query Match
                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Macaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               жив вр
                                                                                                                                                                                                                                                                              RESULT 3
 ន្តដូន
                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                      셤
                                                                                                                                                                 ઠે
                                                                                                                                                                                                                 ò
                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents the heavy chain variable domain of a mutant murine antibody MHM24 of the invention. The mutants are of a species-dependent antibody MHM24 of the invention. The mutants are of a species-variable region of the Ab, and have an amino acid substitution in a non-human mammal at least 10 times stronger than for the wild type Ab against the Ag. The mutant antibodies are particularly intended for administration to a non-human mammal in preclinical studies (e.g. of infection, immunity, haematopolesis or transplantation). They can also be used diagnostically (to identify specific proteins) or therapeutically, e.g. where directed against CDIa (lymphocyte function-associated antigen.) or intercellular adhesion molecule-1 against a wide variety of inflammatory or autoimmune diseases, malignancies transplant rejection, human immune deficiency virus infection and tumour cell invasion. Conversion to the mutant form allows useful antibodies to be produced
                                                                                                                            120
                                                                                                                                        61 NQKPKDRPTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                          9
                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                infection; haematopolesis; lymphocyte function-associated antigen-i; intercellular adhesion molecule-i; inflammatory disease; CDlla; therapy; autoimmune disease; transplant rejection; tumour cell invasion; human immune deficiency virus infection; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mutants of species-dependent antibodies with affinity for non-human mammalian antigen - greater than for parent antibody, particularly used for pre-clinical trial(s) in rhesus monkey(s) of therapeutic antibodies
                                                                                                 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                           61 NOKFKDRFTISVDKSKNTLYLOMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS
                                                                         1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                   Gape
                                                                                                                                                                                                                                                                                                                                                                    Antibody mutant production; species-dependent antibody; malignancy;
                                                   ö
                          Length 121;
                                                 Indels
                        ) Score 649; DB 2;
; Pred. No. 1.7e-49;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                           Murine MHM24 heavy chain variable domain mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 13; Page 59-60; 71pp; English.
                                                                                                                                                                                                                                                                AAW63542 standard, protein; 121 AA.
                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97WO-US020169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96US-00756150
                                                                                                                                                                                                                                                                                                                    (first entry)
                                             Matches 121, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Presta LG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 directed against CD11a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-322726/28.
                                   Similarity
Sequence 121 AA
                                                                                                                                                                           121 S 121
                                                                                                                                                                                                   121 S 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9823746-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-NOV-1996;
                                                                                                                                                                                                                                                                                                                  06-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jardien PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                           AAW63542;
                        Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mue ep.
                                                                                                                                                                                                                                      g
                                                                                                 음
                                                                                                                         ઠે
                                                                                                                                                 셤
                                                                                                                                                                          ઠે
                                                                                                                                                                                                셤
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a humanised anti-CDIIa antibody (Ab) that binds specifically to the human CDIIa I-domain. The Ab has anti-inflasmatory, immunosuppressant, antitumour and antiviral activities. The Ab blocks lymphocyte function-associated antigen (LFA-1) which is involved in leucocyte adhesion associated with inflammatory and immunological responses. The Ab are used: (i) optionally when coupled to a cytotoxin, to treat or prevent disorders mediated by lymphocyte function-associated antigen. (LFA-1; CDIIa/CDI8), e.g. psoriasis, inflammatory bowel disease, eczema, systemic lupus erythematosus, thinties, leukaemia, viral infections and many others, also for timbiting graft rejection; (ii) when labeled, to detect CDIIa; (iii) for tumour pretreatment; (iv) for delivery of enzymes that convert prodrugs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 NQKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                            9
           οĘ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Humanised; anti-CD11a; antibody; anti-inflammatory; immunosuppressant; antitumour; antiviral; inflammation; immunological response; LFA-1; lymphocyte function-associated antigen-1; psortisals; rhinitis; eczema; inflammatory bowel disease; systemic lupus erythematosus; leukaemia; viral infection; transplant rejection; graft rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 NOKFKDRFTISVDKSKNTLYLOMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS
                                                                                                                                                                                                                                                                                                                                    EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                     EVOLVESGGGLVQPGGSLRLSCAASGYSFTGHWMWWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New humanized anti-CD11a antibody, useful for treating or preventing inflammation and transplant rejection, contains human heavy variable region complementarity determining regions.
from antibodies which normally have affinity for non-human analogues the Ag too low to be of any use
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                            Length 121;
                                                                                                                                                                                                                                                         0, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhesusised antibody mutant heavy chain SEQ ID NO:24.
                                                                                                                                                                                     100.0%; Score 649; DB 2;
100.0%; Pred. No. 1.7e-49;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY82348 standard; protein; 121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example, Fig 1; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-00974899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96US-0031971P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                         Matches 121, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jardieu PM, Presta LG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-282241/24.
                                                                                                                                                                                                                          Similarity
                                                                                                                 Sequence 121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mulatta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 8 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 8 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-NOV-1996;
```

```
61 NQKFKDRPTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYPDYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                       61 NOKRYCHTISVDKSKNTLYLOMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                 9
to active anticancer agent; and (v) for affinity chromatography. The Abretain about the same activity in adhesion and mixed lymphocyte response assays as the murine antibodies from which they are derived. The murine anti-CD11a antibody WHM24 has IC50 0.09 mM for preventing adhesion between Jurkat cells (expressing LFA-1) and normal epidermal keratinocytes that express ICAM-1 (intracellular adhesion molecule-1). The fully humanized version of MHM24 had IC50 0.13 nM. The present sequence represents the amino acid sequence of a rhesusised antibody mutant heavy chain, which is used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse; CD11a; I-domain; monoclonal antibody; cluster of differentiation 11a; mixed lymphocyte response assay; cluster cell; epidermal keratinocyte; intercellular adhesion molecule; ICAM-1; lymphocyte function-associated antigen I mediated disorder; psoriasis; Crohn's disease; ulcerative colitis; dermatitis; asthma; rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis; diabetes mellitus; prodrug activating enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Humanized anti-CD11a antibody useful for treating lymphocyte function-
associated antigen mediated disorder e.g. psoriasis, Crohns disease,
ulcerative colitis, dermatitis, asthma, rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                        RVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMWWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                               1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                             ;
o
                                                                                                                                                                                                                                        100.0%; Score 649; DB 3; Length 121; 100.0%; Pred. No. 1.7e-49; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhesusised mouse anti-CD11a I-domain antibody VL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example; SEQ ID NO 24; 43pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADG39012 standard; protein; 121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96US-0031971P.
97US-00974899.
99US-00420745.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2001; 2001US-00795798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                             Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jardieu PM, Presta LG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-051511/05.
                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                         Sequence 121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2003207336-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 S 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 S 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-NOV-1997;
20-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADG39012;
                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADG3901
     8888888888888
                                                                                                                                                                                                                                                                                                                                                 ä
                                                                                                                                                                                                                                                                                                                                                                                                                         윰
                                                                                                                                                                                                                                                                                                                                                                                                                                                               S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                       Ø
```

```
The interior of relaters to a remainisted and the contraction for 50 ft.

A divalue of not more than 1x10-8 M, or concentration for 50 ft.

Inhibition (IC50) (nM) value of not more than 1 nM in mixed lymphocyte response assay or for preventing addression of Jurkat cells to normal human epidermal keratinocytes expressing intercellular adhesion molecule (ICAM).

I. Also included are a kit comprising the antibody and instructions for use to detect the CD11a protein, an isolated nucleic acid encoding the nutleody, a vector comprising the nucleic acid, a host cell so that the antibody is expressed. The antibody binds to epitope MHM24 on CD11a. The antibody is useful for determining the presence of CD1a protein and for treating lymphocyte function-associated antigen I mediated disorder such as psoriasis, Crohn's disease, ulcerative colitis, dermatitis, asthma, rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis and diabetes multipole acid or as an affinity purification agent. The present sequence is the light chain of a rhesusised ant-CD11a antibody of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    adult respiratory distress syndrome; allergic disease; eczema; asthma; autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus; SLB; diabetes mellitus; Reynaud's syndrome; immunological disease; tuberculosis; sarcoidosis; polymyositis; chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder; skin hypersensitivity disorder; poison ivy; poison oak; B-call malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia; graft versus host disease; cancer; gene therapy; murine anti-human CD11a monoclonal antibody; MMM24; variable heavy chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 NOKFKDRFTISVDKSKNTLYLOMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CD11a antibody; human immunodeficiency virus infection; HIV infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMWWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 NQKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVOLVESGGGLVOPGGSLRLSCAASGYSFTGHWMWWRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
relates to a Humanised anti-cluster of differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rhinovirus infection; inflammatory skin disease; psoriasis;
inflammatory bowel disease; Crohn's disease; ulcerative colitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhesusised MHM24 antibody variable heavy chain mutant protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M; murine; rhesus macaque; fusion protein; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 649; DB 8;
100.0%; Pred. No. 1.7e-49;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADR03380 standard; protein; 121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-DEC-2003; 2003US-00727737.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JS2004146507-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mulatta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 S 121
                                                                                                                                                                                                                                                                                                                                                                                              the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 8 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39-JUL-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus sp.
Macaca m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADR03380
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
```

```
Best Local Similarity 96.7
Matches 117; Conservative
                                                                                                                                                                                                          Jardieu PM, Presta LG
                                                                                                                                                       (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                WPI; 1998-322737/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          leukaemia, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 8 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 8 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           409823746-A1.
                                                                                                      27-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-JUN-1998
  04-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW63532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAW63532
  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    XXX2X2X5X5X5XXXXXXXXXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                       The present interaction retactes to an anticology micentic it a special control of the control of a special control of the con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 NOKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 NQKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGGGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                     treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                             New antibody mutant of a species-dependent antibody, useful for thand preventing infectious diseases, psoriasis, inflammatory bowel disease, allergic conditions, autoimmune diseases, or cancer.
                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to an antibody mutant of a species-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complementarity determining region; heavy chain variable region; humanised antibody; MHM24F(ab)-8; anti-CD11a antibody; human CD11a I domain; MHM24 epitope; alpha subunit; lymphocyte function-associated antigen 1; LFA-1; immunoassay; in vivo imaging; diagnosis; CD11a-associated disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heavy chain variable region of humanised anti-CD11a antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 649; DB 8; Length 121; 100.0%; Pred. No. 1.7e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                    Example; SEQ ID NO 17; 54pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW62013 standard; peptide; 121 AA
  96US-0031945P
                        97US-00975329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 121; Conservative
                                                                                                                            Jardieu PM, Presta LG
                                                                        (GETH ) GENENTECH INC
                                                                                                                                                                               WPI; 2004-552640/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 8 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 S 121
27-NOV-1996;
                     20-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ното варіеля
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9823761-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW62013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
```

용

ઠ

셤 ઠે 

```
The present sequence represents the heavy chain variable region of a humanised anti-CDI1a antibody that binds specifically to the human CDI1a I domain (MHM24 epitope). CDI1a refers to the alpha subunit of lymphocyte function-associated antigen I (LPA-1) from any mammal. The humanised anti-CDI1a antibodies are used to determine presence of CDI1a in usual associated by in vivo imaging, particularly for diagnosis of CDI1a associated diseases (typically immune responses and inflammation such as portasis, Crohn's disease, rheumatoid arthritis, transplant rejection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 NOKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 NOKPKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibody mutant production; species-dependent antibody; malignancy; infection; haematopolesis; lymphocyte function-associated antigen-1; intercellular adhesion molecula-1; inflammatory disease; CD11a; therapy; autoimmune disease; transplant rejection; tumour cell invasion; human immune deficiency virus infection; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                       New humanised anti-CD11a antibody - used in immunoassays for CD11a, and also to treat conditions such as immunological or inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.4%; Score 632; DB 2; 96.7%; Pred. No. 5.4e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW63532 standard; protein; 121 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7; Page 50; 66pp; English.
97WO-US019041.
                                                                            96US-00757205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97WO-US020169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96US-00756150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Humanised MHM24 heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
```

ö

```
and was used to produce a mutant of the invention. The mutants are of a species-dependent antibody (Ab), and have an amino acid substitution in a variable region of the Ab, and binding affinity for an antigon (Ag) from a non-human mammal at least 10 times stronger than for the wild type Ab against the Ag. The mutant antibodies are particularly intended for administration to a non-human mammal in preclinical studies (e.g. of infection, immunity, haematopolesis or transplantation). They can also be used diagnostically (to identify specific proteins) or therapeutically, e.g. where directed against CDIIa (lymphocyte function-associated antigen 1) or intercellular adhesion molecule-1 against a wide variety of inflammatory or autoimmune diseases, malignancies, transplant rejection, human immune deficiency virus infection and tumour cell invasion.

from antibodies which normally have affinity for non-human analogues of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 NQKFKDRPTISVDKSKNYILYLQMNSLRABDTAVYYCARGIYFYGTTYPDYWGQGTLVTVS 120
                                                                                                                                                                                                                                                      This sequence represents the heavy chain of the humanised antibody MHM24,
                                                                                                   Mutants of species-dependent antibodies with affinity for non-human mammalian antigen - greater than for parent antibody, particularly used for pre-clinical trial(s) in rhesus monkey(s) of therapeutic antibodies directed against CD1a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Humanised; anti-CD11a; antibody; anti-inflammatory; immunosuppressant; antitumour; antiviral; inflammation; immunological response; LFA-1; lymphocyte function-associated antigen-1; psoriasis; rhinitis; eczema; inflammatory bowel disease; systemic lupus erythematosus; leukaemia; viral infection; transplant rejection; graft rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMWWVRQAPGKGLEWVGMIHPSDSETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 NOKFKDRFTISVDKSKNTLYLOMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Humanised anti-CD11a antibody heavy chain variable region SEQ ID NO:5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 97.4%; Score 632; DB 2; Length 121; Best Local Similarity 96.7%; Pred. No. 5.4e-48; Matches 117; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                             Disclosure; Page 55; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY82336 standard; protein; 121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the Ag too low to be of any use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-00974899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                      Presta LG;
                                                             WPI; 1998-322726/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 S 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 S 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US6037454-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-MAR-2000
                   Jardieu PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY82336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY82336
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ል
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
```

ö

0; Gaps

9 9 120

```
The present invention describes a humanised anti-CD11a antibody (Ab) that binds specifically to the human CD11a I-domain. The Ab has anti-inflammatory, immunosupressant, antitumour and antiviral activities. The Ab blocks lymphocyte function-associated with inflammatory and involved in leucocyte adhesion associated with inflammatory and immunological responses. The Ab are used: (1) optionally when coupled to a cytotoxin, to treat or prevent disorders mediated by lymphocyte function-associated antigen-I (IFA-1; CD11a) (-9. psoriasis, inflammatory bowel disease, eczema, systemic lupus erythematosus, inhibiting graft rejection; (ii) when labeled, to detect CD11a; (iii) for inhibiting graft rejection; (ii) when labeled, to detect CD11a; (iii) for tumour pretreatment; (iv) for delivery of enzymes that convert prodrugs to active anticancer agent; and (v) for affinity chromatography. The Ab ertain about the same activity in adhesion and mixed lymphocyte response assays as the murine antibodies from which they are derived. The murine anti-CD11a antibody MHM24 has IC50 0.09 nM for preventing adhesion between Jurkat cells (expressing IEA-1) and normal epidermal charter express ICAM-1 (intracellular adhesion molecule-1). The fully humanized version of MHM24 had IC50 0.13 nM. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse; CD11a; I-domain; monoclonal antibody; heavy chain variable region; VH; cluster of differentiation 11a; mixed lymphocyte response assay; Jurkat cell; epidermal keratinocyte; intercellular adheaion molecule; ICAM-1; lymphocyte function-associated antigen 1 mediated disorder; psoriasis; Crohn's disease; ulcerative colitis; dermatitis; asthma; rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis; diabetes mellitus; prodrug activating enzyme; humanised.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120
                                                                                                                                                               New humanized anti-CD11a antibody, useful for treating or preventing e.g. inflammation and transplant rejection, contains human heavy variable region complementarity determining regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVOLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Humanised Mouse anti-CD11a antibody heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.4%; Score 632; DB 3; Length 121; 96.7%; Pred. No. 5.4e-48; ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADG38993 standard; protein; 121 AA
                                                                                                                                                                                                                                                    Claim 1; Fig 1; 38pp; English
96US-0031971P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-FEB-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 96.7 Matches 117; Conservative
                                                                                Jardieu PM, Presta LG
                                       (GETH ) GENENTECH INC.
                                                                                                                          WPI; 2000-282241/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 8 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 $ 121
27-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -CD11a Ab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADG38993
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
```

```
C(D) lia antibody having specificity to human CD11a I-domain or CD11a with a kd alue of not more than 1x10-8 M, or concentration for 50 % inhibition (IC50) (nM) value of not more than 1 mM in mixed lymphocyte response assay or for preventing adhesion of Jurkat cells to normal human epidermal keratinocytes expressing intercellular adhesion molecule (ICAM) of the preventing adhesion of Jurkat cells to normal human epidermal keratinocytes expressing intercellular adhesion molecule (ICAM) of the original protein, an isolated nucleic acid encoding the antibody, a vector comprising the nucleic acid, a host cell comprising cantibody, a vector comprising the nucleic acid, a host cell comprising cantibody is expressed. The antibody by culturing the cell so that the antibody is expressed. The antibody by culturing the cell so that the antibody is expressed. The antibody by culturing the cell so that the antibody is expressed. The antibody by culturing the cell so that the antibody is expressed. The antibody by culturing the adiated disorder such as psoriasis, Crohn's alsease, ulcerative colitis, dermatitis, asthma, chemmatoid arthritis, systemic lugue erythematoeus, multiple sclerosis and diabetes mellitus. The antibody is useful when conjugated to a prodrug activating enzyme, or as an affinity purification agent. The present sequence is the heavy chain variable region (VH) of the humanised mouse anti-CD11a I domain monoclonal antibody MHM24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 NOKPKDRFTISVDKSKNTLYLOMNSLRABDTAVYYCARGIYFYGTTYPDYWGGGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 NOKEKDERFIISVDKSKNILYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVIVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                            Humanized anti-CD11a antibody useful for treating lymphocyte function-
associated antigen mediated disorder e.g. psoriasis, Crohns disease,
ulcerative colitis, dermatitis, asthma, rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BVQLVESGGGLVQPGGSLRLSCAASGYSPTGHWWWVRQAPGKGLEWVGMIHPSDSETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EVQLVESGGGLVQPGGSLRLSCAASGYSPTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a Humanised anti-cluster of differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97.4%; Score 632; DB 8; Length 121; 96.7%; Pred. No. 5.4e-48; Live 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7; SEQ ID NO 5; 43pp; English
                                                                                                                                                                                                   96US-0031971P.
97US-00974899.
99US-00420745.
                                                                                                                                                       28-FEB-2001; 2001US-00795798.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 96.7
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                      Jardieu PM, Presta LG;
                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-051511/05.
                                                                 US2003207336-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 8 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 S 121
                                                                                                                                                                                                   27-NOV-1996;
20-NOV-1997;
                                                                                                                                                                                                                                                  20-OCT-1999;
                                                                                                             06-NOV-2003
Synthetic.
                       Mus sp.
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
```

Humanised MHM24 F(ab)-8 antibody variable heavy chain protein. (first entry) 21-OCT-2004 exaxaxa,

ADR03368 standard; protein; 121 AA

RESULT 10 ADR03368 ADR03368

121 S 121

ò

The present invention relates to an antibody mutant of a species—
dependent antibody with beneficial properties. The invention is useful
for treating and preventing infectious diseases such as human
immunodeficiency virus (HIV) and rihinovirus infections, inflammatory skin
disease such as peoriasis, inflammatory bowel diseases such as Crohn's
disease and ulcraritve colitis, adult respiratory distress syndrome,
allergic diseases such as eczema and asthma, autoimmune diseases such as
rheumatoid arthritis, systemic lupus erythematosus (SLB), diabetes
cheumatoid arthritis, polymyositis and chronic obstructive pulmonary
disease (COPD), CNS inflammatory diseases such as
cuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
disease (COPD), CNS inflammatory disease, such as
chronic lymphocytic leuksemia and hairy cell leukaemia, graft versus host
disease and cancer. The invention is also useful in gene therapy. The
present sequence is humanised murine anti-human (Dila monoclonal antibody ö rhinovirus infection; inflammatory skin disease; psoriasis; inflammatory beam disease; croin, s disease; ulcerative colitis; adult respiratory distrass syndrome; allergic disease; eczema; asthma; autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus; SIB; diabetes mellitus; Reynaud's syndrome; immunological disease; cuberculosis; sarcoidosis; polymyositis; chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder; skin hypersensitivity disorder; polson ivy; poison oak; srallyanacy; chronic lymphocytic leukaemia; hairy cell leukaemia; graft versus host disease; cancer; gene therapy; murine anti-human CDIIa monoclonal antibody; MHM24; variable heavy chain; 61 NQKPKORFIISVDKSKONILYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGGGTLVTVS 120 61 NOKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120 New antibody mutant of a species-dependent antibody, useful for treating and preventing infectious diseases, psoriasis, inflammatory bowel disease, allergic conditions, autoimmune diseases, or cancer. 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWANWVRQAPGKGLEWVGMIHPSDSBTRY 60 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWNWVRQAPGKGLEWVGMIAPASSSTRY 60 (MIM24) F(ab)-8 variable heavy chain protein. This sequence is used in CD11a antibody; human immunodeficiency virus infection; HIV infection; Gaps 3, Indels 97.4%; Score 632; DB 8; 96.7%; Pred. No. 5.4e-48; iive 1; Mismatches 3; the exemplification of the invention Example, SEQ ID NO 5; 54pp; English. //H; murine; human; fusion protein. 03-DEC-2003; 2003US-00727737. 96US-0031945P. 97US-00975329. Best Local Similarity 96.7 Matches 117; Conservative Jardieu PM, Presta LG, (GETH ) GENENTECH INC. WPI; 2004-552640/53. JS2004146507-A1. Seguence 121 AA; Homo sapiens. 27-NOV-1996; 20-NOV-1997; 29-JUL-2004 Chimeric. Query Match Мив вр. 셤 ò a Protein purification; leaching; protein A affinity chromatography; CD11a;

24-JUN-2004; 2004US-00877532. 28-JUL-2003; 2003US-0490500P

US2005038231-A1.

Synthetic antibody

17-PEB-2005

Humanized CD11a variable heavy chain amino acid sequence, seq id

```
61 NOKEKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a recombinant monoclonal antibody for human CD11a has the amino acid sequence shown by SEQ ID No.1 or SEQ ID No.5 in light-chain variable region and the amino acid sequence shown by SEQ ID No.2 or SEQ ID No.6 in heavy-chain variable region. Its loactivity and the expression in host cell are greatly increased. The DNA molecule for coding the antibody, its preparation process and the medicinal composition containing it are also disclosed. The present sequence represnts a heavy chain variable region of human CD11a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant human CD11a monoclonal antibody and its preparation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                              monoclonal antibody; CD11a; light-chain variable region; heavy-chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 97.4%; Score 632; DB 8; Best Local Similarity 96.7%; Pred. No. 5.4e-48; Matches 117; Conservative 1; Mismatches 3.
                                                                                                                                                                                                                                                                                                                                                                            (ZHON-) ZHONGXIN GUOJIAN PHARM CO LTD SHANGHAI.
                                                                                                                                                        CD11a heavy chain variable region #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 14-15; 16pp; Chinese.
                                                                     ADW38458 standard; protein; 121 AA
                                                                                                                                                                                                                                                                                                                    20-FEB-2002; 2002CN-00110866
                                                                                                                                                                                                                                                                                                                                                 20-FEB-2002; 2002CN-00110866
                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  medicinal composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-169719/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                        Wang H, Wang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 8 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S 121
121 $ 121
                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                             24-MAR-2005
                                                                                                                                                                                                                                                             CN1439651-A
                                                                                                                                                                                                                                                                                          03-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                   ADW38458;
                                          RESULT 11
                                                           ADW38458
                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
  ď
```

```
The invention relates to a method of purifying a protein which comprises a CH2/CH3 region by protein A affinity chromatography. The method involves reducing the temperature of a composition comprising the protein and one or more impurities subjected to protein A affinity chromatography conditions and one or more impurities subjected to protein A affinity chromatography conditions and one or more impurities subjected to protein A affinity chromatography conditions. The antibody is selected from Trastuzumab, humanized 2C4, humanized CD11a antibody, and humanized VEGF antibody. Preferably, the antibody binds HER2 antigen, where the antibody is preferably and the antibody binds protein is an immunoadhesin, and appricably a protein, which comprises a CH2/CH3 region by protein A affinity chromatography and for reducing leaching of protein A during protein A affinity chromatography. The current sequence represents the protein and animo acid sequence of CD11a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 NOKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 NOKPKORFITISVDKSKNTLYLOMNSLRAEDTAVYYCARGIYFYGTTYFDYWGGGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                    comprises reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 BYOLVESGGGLYOPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Purifying a protein, e.g. antibody or immunoadhesin, comprises reducir. the temperature of a composition subjected to protein A affinity chromatography to 3-20 degrees C, where protein A leaching is reduced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  anti-CD11a rhuMAb heavy chain amino acid sequence #SEQ ID 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Purifying; target protein; non-affinity purification;
                                                                                                                                                                                                                                                                                        ž
                                                                                                                                                                                                                                                                                        Oleary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 632; DB 9;
Pred. No. 5.4e-48;
1; Mismatches 3;
                                                                                                                                                                                                                                                                                        Mcdonald PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 6; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADF11670 standard; protein; 451 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 97.4%;
Best Local Similarity 96.7%;
Matches 117; Conservative
                                                                                                                                                                                                                                                                                          Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                          Laverdiere
                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                           WPI; 2005-172327/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 8 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-FEB-2004
                                                                                                                                                                                                                                                                                             Fahrner RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADF11670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XXXXXXXXXX
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      용
```

ö

9

ö

0; Gaps

9 9

ADX80646 standard; protein; 121 AA.

RESULT 12

ADX80646

(first entry)

05-MAY-2005

ADX80646;

fusion protein.

```
120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mixture containing a host cell protein. This method comprises subjecting the mixture to a non-affinity purification followed by high-performance tangential flow filtration (HPTPP) and isolating the protein in a purity containing less than 100 parts/million (ppm) of the host cell protein, where the method of the invention includes no affinity purification process. The method of the invention is useful for purification protein from a mixture containing a host cell protein, and is useful for purified using the method of the invention are useful in a pharmaceutical respect, and are also useful in various diagnostic and therapeutic purposes. The method of the invention is efficient in purifying a target protein from a mixture containing a host cell protein, and may also be effectively performed at low cost. The current sequence represents the anti-CD11a rhuMAb heavy chain amino acid sequence. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 NOKPKDRFTISVDKSKNTLYLOMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    particular protein was used to demonstrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                     Purifying target protein from mixture containing host cell protein involves subjecting mixture to non-affinity purification, high-performance tangential flow filtration and isolating purified protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 NQKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to a method for purifying a target protein from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWNWWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMWWVQAPGKGLEWVGMIHPSDSETRY
tangential flow filtration; HPTFF; pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibody; humanised; anti-IL-8 monoclonal antibody; interleukin 8; diagnosis; inflammatory disorder; conjugate; immunoglobulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.4%; Score 632; DB 8; Length 451;
llarity 96.7%; Pred. No. 2.1e-47;
Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human IgGl subgroup III heavy chain variable domain.
                                                                                                                                                                                                                                                                                  Van Reis R;
                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 4; 77pp; English.
                                                                                                                                                                                                                                                                                  Lebreton B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY29452 standard; protein; 116 AA
                   diagnostic, therapeutic, antibody
                                                                                                                                                                    25-APR-2003; 2003WO-US013054.
                                                                                                                                                                                                        26-APR-2002; 2002US-0375953P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                Follman D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates
                                                                                                                                                                                                                                         (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                  WPI; 2004-043096/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 117; Conserv
 high-performance
                                                                                        WO2003102132-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 451 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 8 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 S 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-OCT-1999
                                                                                                                             11-DEC-2003
                                                                                                                                                                                                                                                                              Fahner RL,
                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY29452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
```

```
Interleukin-8; IL-8; monoclonal antibody; MAb; anti-IL-8; 6G4.2.5V11N35A; inflammatory disorder; adult respiratory distress syndrome; chimeric; affinity purification; 6G4.2.5.
                                                                                                                                                                                                                                                                                                                                                                conjugates of nonproteinaceous polymers with antibody fragments, used treating inflammatory disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dermatitis, systemic scleroderma and sclerosis, and asthmatic diseases. The conjugates can also be used as reagents in an animal model system for in vivo study of the biological functions of the antigen recognised by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibody fragments covalently attached to one or more nonproteinaceous polymer molecules, where the apparent size of the conjugate is at least about 500 kDs. Conjugates of antibody fragments which bind the human interleukin (IL) 8 with a nonproteinaceous polymer can be used for treating inflammatory disorders e.g. acutel lung injury, ischaemic reperfusion disorder, and autoimmune diseases. They can also be used for treating e.g. inflammatory skin diseases including psoriasis and atopic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 BVQLVESGGGLVQPGGSLRLSCAASGFSFTGHWMWWVRQAPGKGLEWVGMIHPSDSETRY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present sequence represents the human IgG1 subgroup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAARGIYFYGTTYFDYWGQGT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 NOKFKORPTISVDKSKNTLYLQMNSLRAEDTAVYYC-ARGIYFYGTTYFDYWGQGT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      present invention describes a novel conjugate having one or more
                                                                                                                                                                                                                                                                                             Zapata GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84.5%; Score 548.5; DB 2; Length 116; 88.8%; Pred. No. 1.2e-40; ive 2; Mismatches 10; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             III heavy chain variable domain form the present invention
                                                                                                                                                                                                                                                                                             Shahrokh Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human IgG1 subgroup III heavy chain variable domain.
                                                                                                                                                                                                                                                                                             Leong SJ, Presta LG,
                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Fig 29, 360pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY77755 standard; protein; 116 AA
                                                                                                                                                                   98US-00012116.
98WO-US003337.
98US-00121952.
98US-00122513.
                                                                                                                                    99WO-US001081.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 103; Conservative
                                                                                                                                                                                                                                                           (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                             Koumenis I,
                                                                                                                                                                                                                                                                                                                               WPI; 1999-469134/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conjugate. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 116 AA;
                                Homo sapiens.
                                                                  W09937779-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-JUN-2000
                                                                                                                                    19-JAN-1999;
                                                                                                                                                                       22-JAN-1998;
                                                                                                                                                                                                                         24-JUL-1998;
                                                                                                  29-JUL-1999
                                                                                                                                                                                                         24-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY77755;
                                                                                                                                                                                                                                                                                             нвет V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
```

ä

Homo sapiens

JS6025158-A

```
98US-00027449.
            97US-0038664P.
98US-0074330P.
                             Presta LG, Leong SR,
                      (GETH ) GENENTECH INC.
      20-FEB-1998;
             21-FEB-1997;
22-JAN-1998;
15-FEB-2000
```

Gonzalez TN;

New nucleic acid molecule encodes a polypeptide which is an anti-interleukin-8 monoclonal antibody or antibody fragment useful for the production of anti-interleukin-8 monoclonal antibodies or fragments. Example, Fig 29; 188pp; English. WPI; 2000-181809/16.

The invention relates to an anti-interleukin-8 (IL-8) monoclonal antibody (MAD). The anti-IL-8 MAD comprises a sequence containing the CDRs (complementarity determining regions) of the humanized anti-IL-8 6G4.2.5V1N35A light chain; and amino acids 24-253 of the humanized anti-IL-8 6G4.2.5V1N35A heavy chain. The anti-IL-8 MADs and fragments can be used in diagnosis, for affinity purification of IL-8 from recombinant cell culture or natural sources and for the treatment of inflammatory disorders e.g. adult respiratory distress syndrome. Nucleic acids encoding the anti-IL-8 MAD can be associated in a vector with another gene encoding another protein or protein fragment to produce a fusion protein which can make isolation and/or purification of the protein an

Sequence 116 AA;

1; Gaps 84.5%; Score 548.5; DB 3; Length 116; 88.8%; Pred. No. 1.2e-40; tive 2; Mismatches 10; Indels 1 Query Match
Best Local Similarity 88.8
Matches 103; Conservative ò g ሕ

ų

Search completed: April 13, 2006, 17:13:37 Job time: 250.727 secs

THIS PAGE IS BLANK

```
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
```

OM protein - protein search, using sw model

Run on:

April 13, 2006, 17:14:06 ; Search time 25.8908 Seconds (without alignments) 449.666 Million cell updates/sec

Title: Perfect score:

US-10-727-737-17 649 1 EVQLVESGGGLVQPGGSLRL.......PYGTTYFDYWGQGTLVTVSS 121 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Fost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Fatabase :

pir 80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	g heavy	Ig heavy chain V r	g heavy	g heavy chain	g heavy	g heavy chain V	Ig heavy chain - h	g heavy chain -	g heavy	ы	g variable regio	ы	g heavy chain -	g heavy chain V	heavy	g heavy	g heavy	g heavy chain V	g heavy chain	g heavy	heavy chain	g heavy	Ig heavy chain V r						
SUMMARIES	рв ір		2 S31686		2 531588	2 \$26786		2 S31107											2 I55673			_	-		-				2 A47329	
	Length D	125	140	140	140	128	121	119	119	124	143	141	123	120	121	136	120	147	121	123	119	121	132	138	119	117	160	117	118	119
å	Query	71.0	71.0	•	•	70.5		70.1		69.7	69.5	69.4	69.3	69.3	69.0	69.0	68.9	68.8	68.7	68.7	•		68.3	68.3	œ.	•	•	•	۲.	•
	Score	461	461	460.5	459	457.5	457	455	454	452.5	451	450.5	450	449.5	448	447.5	447	446.5	446	446	443	443	443	443	442.5	442	442	441	439	439
	Result No.	-	7	m	4	ß	9	7	60	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

heavy	heavy	heavy	heavy	heavy	heavy	heavy	heavy	heavy	_	heavy chain	heavy	heavy chain	heavy	heavy chain	Ig heavy chain - h
S13791	S36278	831120	AVMST6	H36005	826790	S38489	S31598	S31601	AVMSJS	S20772	S34012	A25912	S31699	S44111	S31117
				٠.	^1										
(V	N	N	_	•••	•••	N	~	~	-	7	N	~	~	~	7
136	120 2	114 2	119 1	121	128	127 2	135 2	130 2	119 1	122 2	•	•		•	122 2
	67.5 120 2										117	139	134	120	
9. 29		67.4	67.4	67.2	67.1	67.0	67.0	6.99	8.99	8.99	66.7 117	66.7 139	66.6 134	66.5 120	

## ALIGNMENTS

```
Query Match
Best Local Similarity
Matches 89; Conserv
                                                                                                                                                                                                                                                                                                                        140 S 140
                                                                                                                                                                                                                                                                                121 8 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                       셤
                                                                                                                                                                                                                          g
                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     合
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fе
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Cross-references: 1-140 ocura
A; Cross-references: UNIPARC; UPI0000116472; EMBL; Z14200; NID; g30957; PIDN; CAA78569.1; PID
C; Superfamily: 1mmunoglobulin V region; 1mmunoglobulin homology
C; Keywords: heterotetramer; 1mmunoglobulin
F; 34-117/ Domain: 1mmunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: S31588
R;Culsinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the A;Reference number: S31588
A;Accession: S31588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: S70442
R;Cuisinler, A.M.; Fumoux, P.; Fougereau, M.; Tonnelle, C.
Mol. Immunol. 29, 1363-1373, 1992
A;Title: IgM kappa/lambda EBV human B cell clone: an early step of differentiation of A;Feference number: S70442; MUID:93024508; PMID:1383695
A;Accession: S70442
                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ä
                                                                                                                                                                                                                            61 NOKPKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARD-HIVGATYFDYWGQGTLVTVS 138
                                                                                                                                           9
                                                                                                                                                                                    79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79
                                                                                                                                                                                                                                                                                                                                                                                                                                                           S70442
Ig heavy chain precursor V region (mu) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 31-Dec-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
                                                                                                                                                              20 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 QVQLVESGGGVVQPGGSLRLSCAASGFTFSNYGMHWVRQAPGKGLEWVAFIRYDGSNKYY
                                                                                                                                       1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EVOLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'Match 71.0%; Score 460.5; DB 2; Length 140; Local Similarity 74.4%; Pred. No. 7e-36; les 90; Conservative 9; Mismatches 21; Indels 1
                                             / Match 71.0%; Score 461; DB 2; Length 140; Local Similarity 73.6%; Pred. No. 6.3e-36; les 89; Conservative 12; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:QBWUK1; UNIPARC:UP10000176EB7
C;Superfamily: immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <1MM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: not compared with conceptual translation
7;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecule type: mRNA
Residues: 1-140 <CUI>
                                                                                                                                                                                                                                                                                                                        121 8 121
                                                                                                                                                                                                                                                                                                                                                                   140 S 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 8 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             139 S 139
                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loc
Matches
                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                          셤
                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                         유
                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
```

```
C'Speciés: Homo sapiens (man)
C'Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C'Accession: S26786
R;Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Bur. J. Immunol. 22, 241-245, 1992
A;Fille: The human cord blood autibody repertoire. Frequent usage of the V(H)7 gene famil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Accession: 526798
R;Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Eur. J. Immunol. 22, 241-245, 1995
A;Fitle: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene famil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPARC:UPI0000115FC5; EMBL:X61014; NID:932800; PIDN:CAA43348.1; PID: C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPARC:UPI0000115FC6; EMBL:X61015; NID:g32795; PIDN:CAA43349.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology < NMM>
                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ä
                                                                                                                                                                                                                                                                      61 NQKPKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYPYGTTYPDYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                        80 ADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCAKDHDYSNYIYFDYWGQGTLVTVS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARGLYCSSTSCYIWSNNWFDPWGQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 NOKFKDRFTISVDKSKNTLYLOMNSLRAEDTAVYYCARGI-----YFYGTTYFDYWGQ 113
                                                                                                                                                                  20 EVQLLESGGGLVQPGGSLRLSCAASGPTPSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY 79
                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLVESGGGLVXPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSSSYTNY 60
                                                                                                                                   BVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 128;
      Length 140,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70.4%; Score 457; DB 2; Length 121;
                                                                 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 70.5%; Score 457.5; DB 2; Best Local Similarity 68.0%; Pred. No. 1.2e-35; Matches 87; Conservative 16; Mismatches 18;
th 70.7%; Score 459; DB 2; Similarity 73.6%; Pred. No. 9.6e-36; B9; Conservative 10; Mismatches 22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig heavy chain V region - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 GTLVTVSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 GTLVTVSS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Accession: S26786
A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-128 <MOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: S26798
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-121 < MOR>
```

ij

120

9

ð

```
C'Species: Homo sapiens (man)
Cjaccesters-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
CjAccession: S23624
R;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.; (J. Exp. Med. 175, 831-842, 1992
J. Exp. Med. 175, 831-842, 1992
A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from tv A;Reference number: S23623; MUID:92156804; PMID:1740665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPARC:UPI0001163EA; EMBL:Z11946; NID:g33897; PIDN:CAA78003.1; PID:C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPARC:UPI000115F94; EMBL:X59703; NID:g32012; PIDN:CAA42224.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C_Species: Homo sapiens (man)
C_JSpecies: Do-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C_JACCession: S20782
R_Mortari, F.; Wang, J.; Schroeder, H.W.
R_Mortari, F.; Wang, J.; Schroeder, H.W.
A_JDescription: Analysis of the IgA and IgG rearranged VH repertoire of human cord blood A_Reference number: S20765
                                                                                                                                                                                                                                                                   61 ADSVKGRPTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDRRLTGT--PDYWGQGTLVTVS 118
                                                                                                                                                        1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 NOKPKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCAR-GIYFYGTT--YFDYWGQGTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ADSVKGRPTISRDNSKNTLYLQMNSLRAEDTAVYYCAKERIAIFGVVIPHFDYWGGGTLV
                                                                                                                                                                                                                                       61 NOKPKORFTISVDKSKNTLYLOMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGEGLEWVST1SGSGDSTYY
                                                                                                                   EVQLVESGGGLVQPGGSLRLSCAASGYSPTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EVOLVESGGGLVOPGGSLRLSCAASGYSFTGHWMNWVROAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3;
                                                                5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 124;
      Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 $; Score 452.5; DB 2; Length

*; Pred. No. 3.4e-35;
11; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
Score 454; DB 2;
Pred. No. 2.4e-35;
9; Mismatches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig heavy chain V region - human (fragment)
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig heavy chain V region - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 72.64
                                                                Conservative
   Query Match
Best Local Similarity
Matches 90; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-124 < MOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: I-143 <OLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 TVSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVSS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                  119 S 119
                                                                                                                                                                                                                                                                                                                                                        121 $ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: S20782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: S23624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                       셤
                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                              유
                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31108
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurmar Bur. J Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A;Reference number: S31104; MUID:92111633; PMID:1730252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C,Accession: S31107
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman B.z. J. Timmers, E.; 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A)Residues: 1-119 -RAA>
A)Cross-references: UNIPARC:UPI0000176DC8; EMBL:X62956
A,Cross-references: UNIPARC:UPI0000176DC8; EMBL:X62956
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin homology rIPM> F;15-98/Domain: immunoglobulin homology cIPM>
                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7
                                                                                                                                                                                                                                           61 ADSVKGRFTISRDNAKNTLYLQLNSLRGEDTAVYYCVRAIGRYSYGYLDYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ADSVKGRPTISRDNSKNTLYLYLQMNSLRAEDTAVYYCAKOPGASY----YPDYWGQGTLVT 116
                                                                                                                                                                                                            61 NQKPKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C_Species: Homo sapiens (man)
C_Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWYRQAPGKGLEWVSAISGSGGSTYY
                                                                                                                          1 EVQLVBSGGGLVQPGGSLRLSCTASGFNFSSHWMHWVRQAPGKGLVWVSHIKYGGTYTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 NOKFKDRFTISVDKSKNTLYLOMNSLRAEDTAVYYCAR--GIYPYGTTYFDYWGQGTLVT
                                                                                        1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EVOLVESGGGLVQPGGSLRLSCAASGYSFTGHWMWWRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 119;
                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.;Residues: 1-119 <RAA>
A.;Cross-references: UNIPARC:UP10000176DC7; EMBL:X62955
   Similarity 71.9%; Pred. No. 1.3e-35; 87; Conservative 7; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 455; DB 2;
Pred. No. 1.9e-35;
9; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70.1%;
Local Similarity 74.0%;
hes 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig heavy chain - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 VSS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 VSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecule type: mRN
                                                                                                                                                                                                                                                                                                                                                                                    121 8 121
                                                                                                                                                                                                                                                                                                                          S 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S31107
Iq heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 91
      Local
                                                                                                                                            끕
                                                                                                                                                                                                            Ġ
                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                 <u>유</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      å
```

à

; ;

8 9 117 120 ä

Gape

6 9

```
Ig heavy chain V region (VH3DJH4) - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Accession: 22-Jan-1993 #sequence_revision 22-Jan-1993 #sequence_revision 22-Jan-1993 #sequence_revision 22-Jan-1993 #sequence_revision 22-Jan-1993 #sequence_revision 22-Jan-1993 #sequence_revision A;Reference number: $19663; MUID:92085276; PMID:1748994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPARC:UP10000116701; EMBL:246382; NID:9562324; PIDN:CAA86521.1; PII CS.Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPARC:UP10000115FB5; EMBL:X61646; NID:g37688; PIDN:CAA43827.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IPM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S48798
R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A;Reference number: S48797
A;Reference number: S48797
A;Reference number: S48798
A;Status: preliminary
                                                                                                                                                                           61 NQKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYF--DYWGQGTLVT 118
                                                                                                                                                                                                        61 ADSVKGRPTISRDNAKNSLYLQMNSLRDEDTAVYYCARSIKYYDENYYGMDVWGQGTTVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 NQKFKDRFŢISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ADSVKGRFTISRDNSKONTLYLOMNSLRAEDTAVYYCAKDRGFW-SGYKDYWGQGTLVTVS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY 60
                                                                                            1 EVOLVESGGGLVQPGGSLRLSCAASGFTFSSYSMWVRQAPGKGLEWVSYISSSSSTIYY
                                                            1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EVOLVESGGGLVQPGGSLRLSCAASGYSFTGHWANWWRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1,
        7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 69.3%; Score 449.5; DB 2; Length Best Local Similarity 73.6%; Pred. No. 6.3e-35; Matches 89; Conservative 11; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 69.0%; Score 448; DB 2; Length 12 Best Local Similarity 71.9%; Pred. No. 8.7e-35; Matches 87; Conservative 12; Mismatches 22; Indels
     22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chain V region (anti-Sm, VH3/Dxp4/JH4b)
     11; Mismatches
     88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Molecule type: mRNA
A, Residues: 1-121 < MAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-120 < MAH>
                                                                                                                                                                                                                                                                                      119 VSS 121
                                                                                                                                                                                                                                                                                                                                             121 VŠŠ 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 8 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: S19666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120
        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            319666
                                                                                                           셤
                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                               ઠ
                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: S26794

R;Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.

Eur. J. Immunol. 22, 21, 245, 1992

A;Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene family. A;Reference number: S26786; MUID:92111632; PMID:1730251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPARC:UP1000011647C; EMBL:214212; NID:g30959; PIDN:CAA78581.1; PIL
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin munoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C'Species: Homo sapiens (man)

C'Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: 831669
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
Bubhitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the A;Reference number: 831585
                                     Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ï
                                                                                                                                                                                                                               61 ADSVKGRFTISRDNAKNSLYLOMNSLRAEDTAVYYCARSGYRGG----DYWGGGGTLVTVS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 ADSVKGRPTISRDNAKNSLYLQMNSLRAEDTAVYYCARGRHLIGEKGYFDLWGRGTLVIV 139
                                                                                                                                                                                                  61 NOKFKDRFTISVDKSKNTLYLOMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-1999
                                                                                                                   1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSNYSMWWRQAPGKGLEWVSYISSSSSTIYY
                                                                                      1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 NOKPKDRPTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYPYGTT-YPDYWGQGTLVTV
                                     4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 450.5; DB 2; Length 141;
; Pred. No. 6e-35;
11; Mismatches 21; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 450; DB 2; Length 123;
Pred. No. 5.8e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPARC:UPI0000176C2B; EMBL:X61011
C;Superfanily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
  74.4%; Pred. No. 5.5e-35; ative 9; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            heavy chain V region - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 73.0%;
Matches 89; Conservative 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig heavy chain V region - human
                               90; Conservative
Best Local Similarity
Matches 90; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: S31669
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-141 <CUI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1-123 <MOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Accession: S26794
A, Status: preliminary
A, Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 SS 121
                                                                                                                                                                                                                                                                                                                121 S 121
                                                                                                                                                                                                                                                                                                                                                                    S 117
                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      쉱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                    ઠે
                                                                                                                                        윱
                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

1,

Gapa

9

ö

Gape

```
RESULT 15
19187

19 Heavy chain V region - human
C;Species: Homo sapiens (man)
C;Accession: S31587
C;Accession: S31587
R;Culsinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
R;Culsinier, A.M.; Gauthier, Johne 1992
R;Culsinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
R;Culsinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
R;Culsinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
R;Culsinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
R;Culsinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
R;Reference number: S31585
R;Reference number: S31585
R;Reference number: S31587
R;Reference number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Cross-references: UNIPARC:UPI0000116468; EMBL:Z14189; NID:931005; PIDN:CAA78558.1; PIC
C,Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;31-114/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ä
                                                                                                                                                                                                                                       61 ADSVKGRPTISRDNSKNTLYLQMNSLRAEDTAVYYCAKTGYSSGWGYPDYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77 VDSVKGRPTISRDNAKNSLYLQMNSLRAEDTAVYYCARGL-TGATDAPDIWGQGTMVTVS 135
                                                                                                                                                                                   61 NOKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 NOKFKORPTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYPDYWGQGTLVTVS 120
1 EVOLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69.0%; Score 447.5; DB 2; Length 172.7%; Pred. No. 1.1e-34; ative 9; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: April 13, 2006, 17:19:34 Job time : 27.8908 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 72.7%
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                      121 8 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 8 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 $ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 $ 136
                                                                                                                                                                                                                                                     ű
                                                                                         셤
                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                             윰
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ቶ
         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ጽ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

## THIS PAGE IS BLANK

```
MOUSE
DOMAIN
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                   removed.
                                                                                                                                         P01807;
                                                                                                                              MOUSE
homo sapien
homo sapien
homo sapien
homo sapien
homo sapien
homo sapien
                                                                                                                                                                                                                                                                                                   rattus norv
mus musculu
rattus norv
                                                                                                                                                                                                                                                                                                                            homo sapien
homo sapien
mus musculu
homo sapien
                                                                                                                                                                                                                                                                                                                                                            homo sapien
mus musculu
homo sapien
homo sapien
                                                                                                                                                                                                                                                                                homo sapien
homo sapien
homo sapien
                                                                                                                                                                                                                                                                                                                      homo sapien
                                                                                                                                                                                                                                                                                                                                                     homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                      homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                            mus musculu
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                        homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                            homo sapien
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          homo sapien
                                                                                                                                                                                                                                                                           mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                      rattus norv
                                           April 13, 2006, 17:05:54 ; Search time 156.93 Seconds (without alignments) 543.993 Million cell updates/sec
                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                  1 EVQLVESGGGLVQPGGSLRL.......FYGTTYFDYWGQGTLVTVSS 121
                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                                                            Q6mzq6
Q924q3
Q6n089
                                                                                                                                                                                                                                                                                Q6gmx2
Q96bb9
                                                                                                                                                                                                                                                                          P01807
      GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                  2166443 seqs, 705528306 residues
                                                                                                                                                                                                                                                                                                                                                                                                  Q6P6C4_HUMAN
Q6MZV7_HUMAN
Q65ZC9_HUMAN
Q96K68_HUMAN
HV07_MOUSE
Q924Q7_MOUSE
                                                                                                                                                                                                                                                                                                   Q4VBH1_RAT
HV38_MOUSE
Q5PQK9_RAT
Q6PJA4_HUMAN
                                                                                                                                                                                                                                                                                                                             Q569F4_HUMAN
Q6P181_HUMAN
HV40_MÕUSE
                                                                                                                                                                                                                                                                                                                                               09UL71 HUMAN
09UL90 HUMAN
09UL91 HUMAN
                                                                                                                                                                                                                                                                                                                                                                        Q6MZŪ6 HUMAN
Q9UL72 HUMAN
Q8WUK1 HUMAN
Q9UL88 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                       HV3D HUMAN
HV41 MOUSE
OSBKIZ RAT
Q6MZQ6 HUMAN
Q924Q3 MOUSE
Q6N089 HUMAN
                                                                                                                                                                                                                                                                                Q6GMX2_HUMAN
Q96BB9_HUMAN
Q6GMX2_HUMAN
                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                  MOUSE
                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                               - protein search, using sw model
                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                       UniProt_05.80:*
1: uniprot_sprot;*
2: uniprot_trembl:*
                                                                                                                                          DB seq length: 0
DB seq length: 200000000
                                                                     US-10-727-737-17
649
                                                                                                                                                                                                                                                       Query
Match Length DB
                                                                                                                                                                                                                                                                                                   67.6
67.4
67.2
66.9
66.9
66.8
                                                                                                                                                                                                                                                                                                                                                             665.0
665.0
665.0
665.0
665.0
                                                                                                                                                                                                                                                                                 428.5
428
                                                                                                                                                                                                                                                                                                                                                                                424.5
424.5
421.5
421.5
421.5
421
421
421
421
420.5
419.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                418
417.5
417
417
                                                                     Title:
Perfect score:
                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                          427
                                OM protein
                                                                                   Sequence:
                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                              Jatabase
                                                                                                                                           Minimum
                                                                                                                                                  Maximum
                                             Eun on:
                                                                                                                                                                                                                                                        Result
                                                                                                                                                                                                                                                               ģ
```

```
This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                      homo sapien
homo sapien
                                                                                                                                                                                                mus musculu
mus musculu
                                                                                                                                                                                                                                                                              homo sapien
homo sapien
                                                                                                                                                                                                                                                                                                                                                           homo sapien
homo sapien
                                             mus musculu
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                         mus musculu
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WICLEOTIDE SEQUENCE OF 1-118.
MEDLINE=90064531; PubMed=2555519;
Miller A. III, Glasel J.A.;
Miller A. III, Glasel J.A.;
"Comparative sequence and immunochemical analyses of murine monoclonal anti-morphine antibodies.";
J. Mol. Biol. 209:763-778(1989).
-! MISCELLANEOUS: This chain was isolated from an IgA myeloma protein that blinds galactan.
-!- SIMILARITY: Contains 1 Ig-like (Immunoglobulin-like) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
19 SEP-2005 (Rel. 48, Last annotation update)
19 heavy chain V region X44.
Mus musculus (Mouse).

Muscupta, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi, Muroidea, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=79223895; PubMed=111245;
Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
Richtural evidence for independent joining region gene in immunoglobulin heavy chains from anti-galactan myeloma proteins and its potential role in generating diversity in complementarity-determining regions.";
Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 119;
                                                                                                                                                                                                                                         0924r8
09y509
06in78
06zvx0
08wu38
0924r3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6xzm9C
                                                                                                                  Q6n096
P01768
                                                                                     2504m7
                                                                                                                                                                                                    Q5£218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13246 MW; BC34FC8F31CD41B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A02077; AVMSX4.
HSSP, P01810; ZFBJ.
SMR; P01807; 1-119.
SMR; P01807; 1-119.
Ensembl; ENSWISGO0000003483; Mus musculus.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SM00406; IGV; I.
PROSITE; PSSO835; IG LIKE; I.
Direct proceeds sequencing; Immunoglobulin domain;
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 442.5;
0901.93_HUMAN
040.924_MOUSE
050.947_MOUSE
0600.96_HUMAN
H736_HUMAN
05.F2_IB_MOUSE
09.24.R8_MOUSE
09.24.R8_MOUSE
06.IN78_HUMAN
06.IN78_HUMAN
06.IN78_HUMAN
06.IN78_HUMAN
10.84.R8_HUMAN
10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q6MZX9 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN SEQUENCE.
```

N

```
121 $ 121
                                                                                                                                                                                                              140 S 140
                                                                                                                                                                                                                                                                                                                                                                    Name=IGHM;
                  Query Match
                                                                                                                                                                                                                                                                     HUMAN
                               Best Loca
Matches
                                                                                                                                                                                                                                                                  RESULT
                                                                                            a
                                                                                                                            ઠ
                                                                                                                                                    셤
                                                                                                                                                                                                        셤
                                                                                                                                                                                   ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Straubberg R.L., Peingol E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Baher N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Baher N.K.,
Altschul R.P., Jordan H., Moore T., Max S.I., Wang J., Hands F.,
Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., McKernan R.J., Makk J.A., Gunzarne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Sheverchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Brown R. Schein J.E., Jones S.J.M., Marra M.A.,
Brown R. Schein J.E., Jones S.J.M., Marra M.A.,
                 3
                                                                                                               61 TPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYCAR-LHYYG--YAAYWGQGTLVTVS 117
                                                                                               61 NOKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                     9
                                                        1 EVKLLESGGGLVQPGGSLKLSCAASGPDFSRYWMSWYRQAPGKGLEWIGEINPDSSTINY
                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                         1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Spleen;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases. |
| Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases. |
| Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases. |
| SMR3, QGGWZ2, 3771; AAH73771.1; -; mRNA. |
| InterPro; IPR003599; Ig. |
| InterPro; IPR003599; Ig. |
| InterPro; IPR003599; Ig. |
| InterPro; IPR003596; Ig. |
| InterPro; IPR003596; Ig. |
| SWART; SW00409; IG; 4. |
| SWART; SW00409; IG; 4. |
| SWART; SW00406; IG; 1. |
| RP0SITE; PS00299; IG. HKF; 4. |
| RP0SITE; PS00299; IG. HKF; 4. |
| SRQUENCE 493 AA; 52865 MW; 55B99305B286203 CRC64; |
 67.8%; Pred. No. 3e-39; stive 19; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
              82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.
                                                                                                                                                                                                                                                     QGGMX2 HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                      IGHAl protein.
Name=IGHAl;
                                                                                                                                                      121 8 121
                                                                                                                                                                                118 A 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Spleen;
                                                                                                                                                                                                                                        HUMAN
              Matches
                                                                                                                                                                                                                         RESULT 2
                                                                                                                                                                                                                                      요
                                                                                                                                                    Š
                                                                                                                                                                             셤
                                                                셤
                                                                                               ò
```

```
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE-22388257; PubMed=12477932; MAX S.I., Wahn G.M., Mahn G.M., Mahn G.M., Mahn G.M., Mahn G.M., Mahn G.M., Mahn M., Sander G.J., Abramson R.D., Millahy S.J., McKernan K.J., Malek J.M., Gay L.J., Hulyk S.M., Makn S.S., Worley K.C., Hale S. Garcia A.M., Gay L.J., Hulyk S.M., Millahon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G., Makeabey R.W., Touchman J.W., Green B.D., Dickson M.C., Makeabey R.W., Touchman J.W., Green B.D., Dickson M.C., Makeabey R.W., Krzywinski M.I., Skalska U., Smailus D.E., Makra M.A., Schhert J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                    ö
                                                                                                                                                                                                                                                                                                 80 ADSVKGRFTISRDNAKNTLYLQMNSLRGEDAAVYYCARGFVSLPRSTLDIWGQGTWVTVS 139
                                                                                                                                                                                                                                                               61 NOKFKDRFTISVDKSKNTLYLOMNSLRAEDTAVYYCARGIYFYGTTYFDYWGOGTLVTVS 120
                                                                                                                                                                                              79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
PubMed=2500644;
Kishimoto T., Okajima H., Okumoto T., Taniguchi M.;
Nucleotide sequences of the CDNAs encoding the V-regions of H- and L-chains of a human monoclonal antibody with broad reactivity to malignant tumor cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                   20 EVQLVESGGGLVQPGGSLRLSCAASGFIFSSYMMHWVRQAPGKGLVWVSRINSDGSSTSY
                                                                                                                                 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                       ö
      Length 493;
                                                                28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
   , DB 2;
1.8e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    597 AA.
Score 442; DB Pred. No. 1.8e 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic Acids Res. 17:4385-0(1989).
EMBL; BCO15760; AAH15760.1; -; mENA.
PIR; SO5271; SO5271.
PIR; S24260; S34260.
HSSP; P01861; 1ADQ.
      68.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2004 (TrEMBLrel. 26, IGHM protein.
                                     71.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q96BB9 HUMAN PRELIMINARY;
Q96BB9;
                              Local Similarity 71.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH MGC Project;
```

```
SMR; Q6GMY2; 20-256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Thymus;
NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q4VBH1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUB-Primary B-Cells;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

METARUBDER R.D., Felingold B.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rutterfield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.B.,

Schnerch A., Schein J.B., Jones B.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 NQKPKDRPTISVDKSKNTLYLQMNSLRAEDTAVYYCA---RGIYFYGT-TYFDYWGQGTL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 ADSVKGRPTISRDNSRDTLYLQMNSLRAEDTAVYYCAKDPRGYSASGNYTREDYWGQGTL 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 EVQLLESGGGLVQPGGSLRLSCAASGFSFSSYAMWWVRQAPGKGLEWVSAISGSGGSTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 BVQLVBSGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           4;
                                                                                                                                                                                                                                                                                                                                                                                     68.1%; Score 442; DB 2; Length 597; 72.8%; Pred. No. 2.2e-38; ive 8; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISCUE-Primary B-Cells;
NIH MGC Project;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073758; AAH73758.1; -; mRNA.
                                                                                                                                                                                                                                                                                        Immunoglobulin domain.
SRQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           606 AA.
                       INTERPRO INTERPROPRIED INTERPR
Ensembl; ENSG0000130076; Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QGGMY2_HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 72.8 tes 91, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 VTVSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 VTVSS 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IGHM protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=IGHM;
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4

IDGGMY2 HU

IDGGMY2 HU

COGMY

COGMY

COGMY

COGMY

COGMY

COGMY

COGMY

COST

COGMY

COST

   RECEERES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
```

```
NEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altausner R.D., Colling F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Antechnok L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Toonlyuki S., Carninci P., Frange C.,
A Brownstein M.J., Usdin T.B., Toonlyuki S., Carninci P., Frange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brichards S., Worley K.C., Hale S., Garca A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glbbs R.A.,
A Packers S., Worley K.C., Hale S., Garchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Schalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Bromerch A., Schein J.E., Jones S.J.M., Marra M.A.,
Bromerch A., Schein J.E., Jones S.J.M., Marra M.A.,
Bromerch A., Schein J.E., Jones B.J.M., Marra M.A.,
Bromerch A., Schein J.E., Jones B.J.M., Marra M.A.,
Bromerch A., Schein J.E., Jones B.J.M., Marra M.A.,
Brownerch A., Schein J.E., Jones B.J.M., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 NOKFKDRFTISVDKSKNTLYLOMNSLRAEDTAVYYCARG--------IYFYG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSSSYTNY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 606;
INTERPRO'S IRROUND'S IG.
INTERPRO'S IRROUND'S IG-like.
INTERPRO'S IG-LIKE.
INTERPRO'S IG-LIKE.
INTERPRO'S IG-LIKE.
INTERPO'S IG-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 68.0%; Score 441.5; DB 2; Length 1 Similarity 63.5%; Pred. No. 2.6e-38; 87; Conservative 14; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       467 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       105 TTYFDYWGQGTLVTVSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 ---MDVWGQGTTVTVSS 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q4VBH1_RAT PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOC299354 protein.
Name=LOC299354;
```

```
PROSITE; PS50835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region.
1 112 Ig-11ke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 S 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Igha protein.
Name=Igha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rissum=Lung;
                                                                                                       NON TER
SEQUENCE
                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OS POR PORT OF PROPERTY OF PRO
                                                                                                                                                                                                                                                                                                                                                                                                                  q
          STTTS
                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 NQKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTY-FDYWGQGTLVTV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 PDSVKGRFTISRDNAENTVYLQMNSLRSEDTATYYCAKGGEYYGYNYPFDYWGQGVWVTV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 EVQLVETGGGLVQPGRSLKLSCVASGFTFSSYMMYWIRQAPGKGLEWVSSINTDGGSTYY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 BVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rao D.N., Rudikoff S., Krutzsch H., Potter M., Structural evidence for independent joining region gene in "Structural evidence for independent joining region gene in immunoglobulin heavy chains from anti-galactan myeloma proteins and its potential role in generating diversity in complementarity-determining regions ", perc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).

-I-MISCELLANEOUS: This chain was isolated from an IGA myeloma protein that binds galactan.
                         C -1 FUNCTION: Beca-2 microglobulin is the beta-chain of major histocompatibility complex class I molecules (By similarity).
-1 SUBCELLULAR LOCATION: Secreted (By similarity).
R EMBL; BC055846; AAH95846.1; -; mRNA.
R InterPro; IPR003159; Ig.
R InterPro; IPR003159; Ig.
R InterPro; IPR003159; Ig.
R InterPro; IPR003159; Ig.
R Pfam; PR07654; Claset; 3.
R Pfam; PR07654; Claset; 3.
R PART; SM00409; IG.; 2.
SMART; SM00406; IG.; 2.
R SMART; SM00406; IG. 1.
R PR0511E; PS50815; IG. LIKE; 4.
R PR0511E; PS50815; IG. LIKE; 4.
R Mmunoglobulin domain; Repeat.
C SEQUENCE 467 AA, 51651 MW; IPP0328P50160ED3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                       67.6%; Score 438.5; DB 2; Length 67.2%; Pred. No. 4e-38; ative 14; Mismatches 25; Indels
       Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A02078; AVMST6.
HSSP: P01810; 2FBJ.
SMR; P01808; 1-119.
Ensembl; ENSMUSG0000003483; Mus musculus.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR0075596; Ig-v.
SMART; SM00406; IGV; II-v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=79223895; PubMed=111245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig heavy chain V region T601. Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 88 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 SS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HV38 MOUSE
P01808;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  removed.
       요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

```
MULDIALING SEMULATION SEMULATION SEMULATION SEMULATION SEMULATION SEMULATION SEMULATION SEMILATION WE STANDARD SEMILATION WE STREAMBOR S. WE STANDARD S. WE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 NQKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 TPSLKDKPIISRDNAKNTLYLQMSKVRSEDTALYYCAR-LGYYG--YFDVWGAGTTVTVS 117
                                                                                                                                                                                                                                                                                                                                                                                                        1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
Bukaryota, Mecazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butcharia; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                  3; Gaps
                                                                                                                                           ch 67.4%; Score 437.5; DB 1; Length 119; Similarity 67.8%; Pred. No. 1e-38; 82; Conservative 17; Mismatches 19; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC087137; AAH87137.1; -; mRNA.
119 119 119 119 MW; BC38CC84E6EA00E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; BC087137; AAH87137.1; -; mRNA.
GO; GO:0003823; F:antigen binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001599; IG.
InterPro; IPR007110; IG-like.
InterPro; IPR003597; IG_C1.
InterPro; IPR003006; IG_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QSPOK9 RAT PRELIMINARY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q5PQK9;
01-FEB-2005 (TrEMBLrel.
01-FEB-2005 (TrEMBLrel.
01-FEB-2005 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH MGC Project;
```

```
IPR007110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IGHG1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 S 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 S 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=IGHG1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse
                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0569F4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
026 6874 HUI
11D 026 9 HUI
11D 026 9 HUI
11D 026 9 HUI
11D 11D HUI
11D 126 9 HUI
11D 126 HUI
126 HUI
127 HUI

       88888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUB-Primary B-Cells,

TISSUB-Primary B-Cells,

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Retaubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Riauserg R.L., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsich F.,

Brownstein M.J., Usdin T.B., Farmer A.A., Rubin G.M., Hong L.,

Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., WcKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Iu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                       61 NQKFXDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQCTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                           80 PDSVKGRFTISRDNAKSTLYLQMNSLRSEDTATYYCTRAAHVMGPYYFAYWGQGVMVTVS 139
                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                       20 EVQLVESGGGLVQPGRSLKLSCVASGFSFNNYMMTWIRQAPGKGLEWVASITNTGGKTYY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                              1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                             67.2%; Score 436; DB 2; Length 479; 66.9%; Pred. No. 7.6e-38; ive 9; Mismatches 31; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC018747; AAH18747.1; -; mRNA.
HSSP; P01861; 1ADQ.
InterPro; IPR003596; Ig v.
Pfam; PR07654; C1-set; 2.
SMART; SM00409; IG; 3.
SMART; SM00400; IG; 3.
SMART; SM00406; ICv; 1.
PROSITE; PS50835; IG LIKE; 3.
PROSITE; PS00290; IG MC; UNKNOWN 2.
SRQUENCE 479 AA; 52354 MW; 1692EP3457BE686E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
IGHG1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   470 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QEPJA4 HUMAN PRELIMINARY;
QEPJA4;
                                                                                                                                                                                                                                        Best Local Similarity 66.9
Matches 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003599; Ig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
TISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH MGC Project;
Submitted (DEC-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 S 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 S 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMR; Q6PJA4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=IGHG1
                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          机械放射器 医环境
                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                       5
                                                                                                                                                                                                                                                                                                                                                                                                                                              G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               욢
```

```
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Rlausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., WcKernan K.J., Mallek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Multing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield X.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Brownster D.N., Schmitz J.M., Marra M.A.,
Schmerch A., Schmit Lital analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 EVQLVESGGGLVQPGGSLRLSCVVSGFTFSSYWMS#VRQAPGKGLE#VANIKQDGSEKYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH MGC Project;
Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BC092518; AAH92518.1; -; mRNA.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003066; Ig_rMC.
InterPro; IPR003066; Ig_v.
Pfam; PF07654; C1-8et; 3.
SMART; SM00409; IG; 2.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS002309; IG_MIC; UNKNOWN 2.
SRQUENCE 470 AA; 51716 MW; 7B49556A11PD7D99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                             67.0%; Score 435; DB 2;
70.2%; Pred. No. 9.5e-38;
iive 9; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last seq
10-MAY-2005 (TrEMBLrel. 30, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q569F4 HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 70.2
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequences.
```

```
Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             binds galactan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Davies D.R.;
                                  PROSITE;
SEQUENCE
      PROSITE;
                                                                                                                                    Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HV40_MOUSE
                                                                                                                                                                                                         Matches
   8 8 8
8
                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                         요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIDDEN BENEFIT THE SECOND OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE—Frimary B-Cells,

RELINE=22388257, PubMed=12477932; DOI=10.1073/pnas.242603899;

RETAUSDERGR R.L., Peringold B.A., Grouse L.H., Derge J.G.,

RIJUBRIER R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

RIJUBRIER R.P., Jordan H., Moore T., Max S.I., Wang J., Haich F.,

Diatchenco L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rabla S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robat S.A., McEwan P.J., McKernan K.J., Male J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rable D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rable J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rablesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S. M., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield A., Schein J.E., Jones S.J.M., Marra M.A.,

Roberzation and initial analysis of more than 15,000 full-length human
                                                                                                                                       ?
                                                                                                                                                                                                                                                                                                                                   61 NQKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCA-RGIYFYGTTYFDYWGQGTLVTV 119
                                                                                                                                                                                                                                                                                                                                                                         80 ADSVKGRFTISRDNSKNSLYLQMNSLRAEDTALYYCATRG--GYSTAGFDYWGQGTLVTV 137
                                                                                                                                                                                                                                        20 EVQLVESGGVVVQPGGSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSLISWDGGSTYY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nomo Partena Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae;
                                                                                                                                                                                                  1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                    .
.
                                                              66.9%; Score 434.5; DB 2; Length 469; 73.0%; Pred. No. 1.1e-37; ative 9; Mismatches 21; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC041037; AAH41037.1; -; mRNA.
HNSP; P018G1; 1ADQ.
INTERPO: IPRO013599; IG.
INTERPO: IPRO013599; IG.
INTERPO: IPRO03599; IG.
INTERPO: IPRO03599; IG.
INTERPO: IPRO03596; IG.
INTERPO: IPRO03596; IG.
INTERPO: IPRO03596; IG.
SMART; SMO0409; IG.; 2.
SMART; SMO0406; IG.; 3.
SMART; SMO0406; IG.; 1.
469 AA; 51254 MW; AC13448E3047784F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.";
proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QEPIB1_HUMAN PRELIMINARY;
                                                                                                                                    89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
TISSUE=Primary B-Cells;
NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE
                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 SS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138 88 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GHM protein.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26PI81,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
06 P181 HUM
10 P6 P181 HUM
10 P6 P181 HUM
10 P5 JUU
10 P
                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                               ò
```

```
This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A02080; AVMSJ5.
PDB; ZFBJ; X-ray; H=1-119.
SMR; P01810; 1-119.
SMR; P01810; 1-119.
INCORPOSO0000003483; Mus musculus.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003596; Ig-v.
SMRT; SM00406; IGv; 1.
PROSITE; PSS0815; IG IKK; 1.
3D-structure; Direct_protein sequencing; Immunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                                                                61 NOKFKDRFTISVDKSKNTLYLOMNSLRAEDTAVYYCARGI-----YFYGTTYFDY 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 VDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREFESTWTTVNADYYY--FYMDV 137
                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The galactan-binding immunoglobulin Fab J539: an X-ray diffraction study at 2.6-A resolution.";
Proteins 1:74-80(1986).
-I- MISCELLANEOUS: This chain was isolated from a myeloma protein that
                                                                                                                                                                                                                                                                             1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                    20 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYMMSWVRQAPGKGLEWVANIKQDGSEKYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HV40_MOUSE STANDARD; PRT; 119 AA.
P01810;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Ig heavy chain V region J539.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchoncoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-79223895; PubMed-111245; Rao D.N., Rudikoff S., Krutzach H., Potter M.; Rad D.N., Rudikoff S., Krutzach H., Potter M.; Extructural evidence for independent joining region gene in immunoglobulin heavy chains from anti-galactan myeloma proteins and its potential role in generating diversity in complementarity-determining regions."; Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894 (1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-TAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
MEDLINE-88217852; PubMed=3449853; DOI=10.1002/prot.340010112;
Suh S.W., Bhat T.N., Navia M.A., Cohen G.H., Rao D.N., Rudikoff S.,
                                                                                                                                                                                                             12;
                                                                                                                                      Length 478;
                                                                                                                                                                                                             23; Indels
PS50835; IG LIKE; 4.
PS00290; IG MHC; UNKNOWN 2.
478 AA; 52667 MM; 17BED38D917970D6 CRC64;
                                                                                                                                      66.9%; Score 434; DB 2;
66.4%; Pred. No. 1.2e-37;
iive 9; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY PROTEIN SEQUENCE
                                                                                                                                                                                                          87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138 WGKGTTVTVSS 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 WGOGTLVTVSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunoglobulin V region.

NON TER 119 119

STRAND 3 7

STRAND 10 12
```

```
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                            JT 13
90 HUMAN
QOUL90 HUMAN PRELIMINARY;
QOUL90;
                                                                                                                                                                                        Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
                                                                   117 VTVSS 121
                                                                                   117 VTVSS 121
                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 S 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 $ 113
                                                                                                                                                                                 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                 ò
                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ñ
                                                                                                                                                                                                                         61 NOKPKORFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                                                                                                                                                                                   9
                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                         1 EVOLVESGGGLVQPGGSLRLSCAASGYSPTGHWWNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                   1 EVKLLESGGGLVQPGGSLKLSCAASGFDFSKYWMSWVRQAPGKGLEWIGEIHPDSGTINY
                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.",
                                                                                                                                                                         .,
,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8;
                                                                                                                                                       66.8%; Score 433.5; DB 1; Length 119; 66.1%; Pred. No. 2.8e-38; ive 20; Mismatches 18; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66.7%; Score 433; DB 2; Length 121; 69.6%; Pred. No. 3.2e-38; ive 11; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                       13240 MW; 577B4F1DB675C1F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cin. Immunol. Immunopathol. 87:184-192 (1998).
EMBL; AR035043; AAD56279.1; -; mRNA.
HSSP; P01852; INPD.
SMR; O9UL71; 1-121.
Ensembl; ENSG0000130076; Homo sapiens.
InterPro; IPR007110; 19-1ike.
InterPro; IPR007110; 19-1ike.
InterPro; IPR001596; Ig-v.
SMART; SM00406; IGv; 1.
NON TREE PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                         121 AA
                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 69.6%
Matches 87; Conservative
                                                                                                                                                                        80; Conservative
                                                                                                                                                                                                                                                                                                                         Q9UL71 HUMAN PRELIMINARY;
121
                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
                                                                                                                               112 1
119 AA;
                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     MCBI_TaxID=9606;
 118 A 118
                                                                                                                                                                                                                                                              121 S 121
                                          STRAND
TURN
STRAND
TURN
STRAND
HELIX
STRAND
HELIX
STRAND
STRAND
STRAND
STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               foung D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON TER
NON TER
                                                                                                                                                                                                                                                                                                                 HUMAN
TURN
STRAND
HELIX
STRAND
                                                                                                                                                                  Best Loca
Matches
                                                                                                                                                                                                                                                                                                                         음
                                                                                                                                                                                                                                            å
                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                              ş
                                                                                                                                                                                                                                                                             셤
```

```
ä
                                                                                                                                                                            61 ADSVKGRFTISRDNSKNSLYLQMNSLRAEDTALYYCAKGKVTTIY----DRPDIWGQGTM 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 NOXFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ADSVKGRPTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDL------NYWGQGTLVTVS 112
                                                                                                                                       61 NOKFKORFTISVDKSKNTLYLOMNSLRAEDTAVYYCARG----IYFYGTTYFDYWGQGTL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=1730252;
Raaphorst F.M., Timmers E., Kenter M.J., Van Tol M.J., Vossen J.M., Schuurman R.K.;
Schuurman R.K.;
Schuurman R.K.;
Restricted utilization of germ-line VH3 genes and short diverse third complementarity-determining regions (CDR3) in human fetal B lymphocyte immunoglobulin heavy chain rearrangements.";
EMBL; APO35024; AAD56260.1; -; mRNA.
EMBL; APO35024; AAD56260.1; -; mRNA.
HSSP; PO1772; 2FB4.
SNR; Q9UL90; 1-113.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                    1 EVQLVESGGGVVQPGGSLRLFCAASGFTFDGYAMHWVRQAPGKGLEWVSLISGDGGSTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MUCLECTIDE SEQUENCE.
MEDLINE-98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 66.1%; Score 429; DB 2; Length 11 Similarity 70.2%; Pred. No. 8e-38; 85; Conservative 10; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in. Immunol. Immunopathol. 87:184-192(1998).
```

```
DOMAIN
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                          removed
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ሯ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                 Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 BVQLVBSGGGLVQPGGSLRLSCAASGFTFSSYSMWWRQAPGKGLEWVSYISSTIIITYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                           Manheimer-Lory A., Katz J.B., Pillinger M., Ghossein C., Smith A.,
                                                                                                                                                                                                                                                                                                                     Makiya R., Stigbrand T., "Placental alkaline phosphatase has a binding site for the human immunoglobuline of protrion."; Bur. J. Blochem. 205:341-345[1992].
EMBL, AF035023; AAD56259.1; -; mRNA.
                                                                                                                                                                                 Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ñ
                                                                                                                                                    MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.0%; Score 428.5; DB 2; Length 118; 70.8%; Pred. No. 9.5e-38; ive 10; Mismatches 22; Indels 3
                                                                                                                                                                                                                                                     Diamond B.;
"Molecular characteristics of antibodies bearing an anti-DNA-
associated idiotype.";
J. Exp. Med. 174:1639-1652(1991).
                                  118 118
118 AA; 12843 MW; D0633949F2AC149D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
19 heavy chain V region X24.
Mus musculus (Mouse).
                  118 AA.
                                                                                                                                                                                           fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 AA
                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50835; IG LIKE; 1.
               Q9UL91 HUMAN PRELIMINARY;
Q9UL91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 70.84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                   PIR, PHO875; PHO875.
PIR, S21205; S21205.
PIR, S30531, S30531.
HSSP, PO1783; IJGC.
SMR, Q9UL91; 1-117.
                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
                                                                                                                                             NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                    PROTEIN SEOUENCE.
                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                             PubMed=1555592;
                                                                                                                                                                         Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HV39 MOUSE
P01809;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
HV39 MOUSE
AC PO1809 DT 21-JUL-
DT 21-JUL-
DT 13-SEP-
DE 19 heav
                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
```

```
This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MUCLEOTIDE SEQUENCE OF 103-117.

MEDLINE=92355114; PubMed=1644448; DOI=10.1007/BF00215659;

Solin M.L., Kaartinen M.;

"Allelic polymorphism of mouse Igh-J locus, which encodes immunoglobulin heavy chain joining (JH) segments.";

Immunogenetics 36:306-313(1992).

-I- MISCELLANEOUS: This chain was isolated from an IgA myeloma protein that binds galactan.

-I- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutharia, Buarchontoglires, Glires, Rodentia, Sclurognathi,
Murcides, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 BVKLLESGGGLVQPGGSL-LSCAASGPDFSRYWMSWARQAPGKGQEWIGEINPGSSTINY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Gaps
                                                                                                                                                                                        MEDLINE=79223895; PubMed=111245;
Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
"Structural evidence for independent joining region gene in immunoglobulin heavy chains from anti-galactan myeloma proteins and its potential role in generating diversity in complementarity-determining regions.";
Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 AA; 13105 MW; BB16A2DB677EF17F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, X63164; -; NOT_ANNOTATED_CDS; Genomic_DNA.
PIR; PT0394; AVMSX2.
HSSP; P01810; 2FBJ.
SWR; P01809; 1-118.
Ensembl; ENSWUSG0000003483; Mus musculus.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-like.
PR051TF; SM04406; IGV; I-PR051TF; PS50835; IG_LIKE; I.
Direct protein sequencing; Immunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.9%; Score 428; DB 1; 66.9%; Pred. No. 1.1e-37; iive 17; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: April 13, 2006, 17:18:40 Job time : 158.93 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                PROTEIN SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 S 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 8 117
```

Appl

Sequence Sequence

ALIGNMENTS

Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence Sequence Sequence Sequence

Sequence

Seguence

```
EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EVOLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 649; DB 3; Length 121; 100.0%; Pred. No. 7.8e-52; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DAN Way
CITY: SOUTH San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                  US-110-922-651-4
US-110-861-049-4
US-110-021-874-4
US-111-021-874-4
US-03-726-258-52
US-09-726-258-55
US-09-726-258-71
US-09-726-258-71
US-09-726-258-71
US-09-726-258-71
US-09-726-258-71
US-09-726-258-71
US-09-811-123-2
US-10-608-501-4
US-10-608-526-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION NUMBER: 08/974,899
FILING DATE: CUNCHOWN:
APPLICATION NUMBER: 08/974,899
FILING DATE: CUNCHOWN:
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/252-981
INFORMATION FOR SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-795-798-24
; Sequence 24, Application US/09795798
; Publication No. US20030207336A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 121 amino acide TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 121; Conservative
7799.66

7799.66

7799.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

7755.00

775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-795-798-24
   4899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Appli
Sequence 5, Appli
Sequence 4, Appli
Sequence 50, Appl
Sequence 50, Appl
Sequence 46, Appl
Sequence 46, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Appl
Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 24, App.
Sequence 17, App.
                                                                                                                                                                                                                                                                                                      (without alignments)
425.257 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20, Sequence 46, Sequence 46, Sequence 2, Sequence 2, Sequence 14, Sequence 14, Sequence 2, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EVQLVESGGGLVQPGGSLRL......PYGTTYPDYWGQGTLVTVSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                                                                               April 13, 2006, 17:19:49 ; Search time 118.886 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
                                       GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-795-798-24
US-10-727-737-17
US-10-727-737-17
US-10-727-737-5
US-10-877-532-6
US-10-873-299-4
US-10-835-641-20
US-10-835-641-20
US-10-813-641-20
US-10-813-641-20
US-10-81-049-46
US-10-81-049-14
US-11-005-677-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Published Applications AA Main:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1867569 segs, 417829326 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                US-10-727-737-17
649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                548.5
520.5
517.5
517.5
517.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
516.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Searched
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database
                                                                                                                                                                                                                                                                           Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Result
No.
```

ö 9 9

0; Gaps

```
US-09-795-798-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                61 NOKPKORFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                           61 NQKEKDRPTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 NOKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 NQKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGGGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 649; DB 4; Length 121; Best Local Similarity 100.0%; Pred. No. 7.8e-52; Matches 121; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winbatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/727,737
FILING DATE: 03-Dec-2003
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/975,329B FILING DATE: 20-N0v-1997
APPLICATION NUMBER: 60/031945
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
REGISTRAION NUMBER: 40,378
                                                                                                                                                                                                                                 Sequence 17, Application US/10727737
Publication No. US20040146507A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Antibody Mutants
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: P1064R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: Linear SEQUENCE DESCRIPTION: SEQ ID NO: 17: US-10-727-737-17
                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 121 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 17
                                                                                             121 $ 121
                                                                                                                                   121 8 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 8 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 S 121
                                                                                                                                                                                                                  US-10-727-737-17
                                                                                                                                                                                                 RESULT
                ઠે
                                                    윱
                                                                                             ઠે
                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
```

RESULT 3

```
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 NOKFKDRFTISVDKSKNTLYLOMNSLRAEDTAVYYCARGIYFYGTTYFDYWGOGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 NQKFKDRPTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EVQLVESGGGLVQPGGSLRLSCAASGYSPTGHWMNWVRQAPGKGLEWVGMIHPSDSETRY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
97.4%; Score 632; DB 3; Length 121;
Best Local Similarity 96.7%; Pred. No. 2.8e-50;
Matches 117; Conservative 1; Mismatches 3; Indels
Sequence 5, Application US/09795798
Publication No. US20030207336A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBW PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRITY APPLICATION NUMBER: US/09/795,798 FILING DATE: 28-Feb-2001 CLASSIPICATION OF CURROWN-PRIOR APPLICATION NUMBER: US/09/795,798 FILING DATE: 28-Feb-2001 CLASSIPICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: 08/974,899 FILING DATE: CUNKNOWN-ATTORNEY/AGENT INFORMATION: NAME: Lee, Wendy M. REGISTRATION NUMBER: 40,378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/10727737
Publication No. US20040146507A1
GENERAL INFORMATION:
I TITLE OF INVERTION: Antibody Mutants
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                          ADDRESSEE: Genentech, Inc. STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 121 amino acide
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 650/952-9891
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 $ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 S 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-795-798-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-727-737-5
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                            61 NQKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYXCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 NQKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 NOKFKURFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                         61 NOKFKDRFTISVDKSKNTLYLOMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIHPSDSETRY
                                                                                                                                1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIHPSDSETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                              Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 50, Application US/09726258
Publication No. US20030021790A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Heei, Vanessa
APPLICANT: Koumenis, Iphigenia
APPLICANT: Feeta, Leonar R.
APPLICANT: Presta, Leonar G.
APPLICANT: Shahrokh, Zahra
APPLICANT: Sapta, Gerardo A.
APPLICANT: Sapta, Gerardo A.
ITLE OF INVENTION: ANTIBODY PRAGMENT-POLYMER CONJUGATES AND
TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/10423299;
Sublication No. US2003022212A1
GENERAL INFORMATION:
APPLICANT: FOLLMAN, DEBORN
APPLICANT: FOLLMAN, DEBORN
APPLICANT: FOLLMAN, DEBORN
APPLICANT: LEBRETON, BRNEDICTE
APPLICANT: LAND REIS, ROBERT
TILLS OF INVENTION: NON-APPINITY PURIFICATION OF PROTEINS
FILE REFERENCE: 39766-0121A
CURRENT APPLICATION NUMBER: US/10/423,299
CURRENT APPLICATION NUMBER: US 60/375,953
PRIOR APPLICATION NUMBER: US 60/375,953
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 4
LENGTH: 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 97.4%; Score 632; DB 4; Length 451; Best Local Similarity 96.7%; Pred. No. 1.1e-49; Matches 117; Conservative 1; Mismatches 3; Indels
Best Local Similarity 96.7%; Pred. No. 2.8e-50; Matches 117; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: Sequence is synthesized US-10-423-299-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech
                                                                                                                                                                                                                                                                                           S 121
                                                                                                                                                                                                                                                                                                                                            121 S 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 8 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 8 121
                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            硆
                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INPORMATION:
APPLICANT: PARRINER, ROBERT L.
APPLICANT: LAVERDIERE, ANY
APPLICANT: LAVERDIERE, ANY
APPLICANT: MOUNDALD, PAUL
APPLICANT: O'LEARY, RHONA M.
TITLE OF INVENTION: REDUCING PROTEIN A LEACHING DURING PROTEIN A AFFINITY CHROMATOGRA
TILLE REFERENCE: P2015R1
CURRENT APPLICATION NUMBER: US/10/877,532
CURRENT FILING DATE: 2004-06-24
RELOR APPLICATION NUMBER: US 60/490,500
PRIOR FILING DATE: 2003-07-28
NUMBER OF SEQ ID NOS: 8
SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 NOKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 NOKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    မ္မ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIHPSDSETRY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.4%; Score 632; DB 4; Length 121;
96.7%; Pred. No. 2.8e-50;
tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.4%; Score 632; DB 5; Length 121;
                     COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 1BM PC compatible COFRUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winbatin (Genettech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,737
FILING DATE: 03-Dec-2003
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/975,329B
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 60/031945
FILING DATE: 27-NOV-1996
ATTORNEY/ABGINT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Lee, Wendy M.
REGISTRATION UNMER: 40,378
REPERENCE/DOCKET NUMBER: P1064R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; FRATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-877-532-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-727-737-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 121 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/10877532 Publication No. US20050038231A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 96.79
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 S 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 $ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-877-532-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
```

셤

ò g ò

```
61 NQKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTT--YFDYWGQGTLVT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 NQKPKDRFTISVDKSKNTAYLQMNSLRAEDTAVYYCARSGY-YGDSDWYFDVWGQGTLVT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGYTMNWVRQAPGKGLEWVALINPYKGVSTY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EVQLVESGGGLVQPGGSLRLSCAASGYTFTSYNMHWVRQAPGKGLEWVGAIYPGNGATSY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ALGORITHON THE APPLICANT: APPLICANT: Olan Gong APPLICANT: Olan Gong APPLICANT: Olan Gong APPLICANT: Playius Martin TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS FILE REFERENCE: P2040RIUS CURRENT PLICATION NUMBER: US 60/476,531 PRIOR APPLICATION NUMBER: US 60/476,531 PRIOR APPLICATION NUMBER: US 60/476,481 PRIOR APPLICATION NUMBER: US 60/476,481 PRIOR PELLON DATE: 2003-06-05 PRIOR FILING DATE: 2003-06-05 PRIOR FILING DATE: 2003-06-05 NUMBER OF SEQ ID NOS: 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.7%; Score 517.5; DB 5; Length 452; 82.0%; Pred. No. 3.4e-39; tive 8; Mismatches 13; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 5; Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 520.5; DB 5; Length
Pred. No. 4.8e-40;
4; Mismatches 13; Indels
                                                                                                                                                                                                     REGISTRATION NUMBER: 40,378
REPERBINGE/DOCKET NUMBER: P0709PID2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEPAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
               APPLICATION NUMBER: US/09/705,398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: sequence is synthesized
                                   FILING DATE: 02-Nov-2000
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M:
                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 46, Application US/10861049; Publication No. US20050095243A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 122 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 83.77
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 82.0
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 VSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-861-049-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-835-641-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-861-049-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EVQLVESGGGLVQPGGSLRLSCAASGFSFTGHWMWWYRQAPGKGLEWVGMIHPSDSETRY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.5%; Score 548.5; DB 3; Length 116;
88.8%; Pred. No. 1.2e-42;
.ive 2; Mismatches 10; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAARGIYPYGTTYFDYWGQGT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 NOKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYC-ARGIYFYGTTYFDYWGQGT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Carter, Paul J.
Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Wilbatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/835,641

FILING DATE: 30-Apr-2004

CLASSIFICATION DATA:

PRIOR APPLICATION DATA:
                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                            PILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 60/094003
PILING DATE: 24-UUL-1998
ATTONBY/AGENT INFORMATION:
NAME: Love, Richard B. 659
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 91085R4-1A
TELECOMMUNICATION INPORMATION:
TELEPHONE: 650/252-5530
                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winparin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/726,258
FILING DATE:
                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/234,182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20, Application US/10835641
Publication No. US20040236078A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
F: 1 DNA Way
South San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 116 amino acida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 88.8°
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: Linear
                                                                                 USA
                                                                                                          94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-726-258-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-835-641-20
                                                                              COUNTRY:
```

셤

ઠે

셤

ઠે

```
i PEATURE:
i OTHER INFORMATION: humanized sequence
US-10-818-765-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Artificial sequence
                                                                                      Query Match 79.6
Best Local Similarity 82.0
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 79.6
Best Local Similarity 82.0
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                  120 SS 121
                                                                                                                                                                                                                                                                                                                                                                                              ||
|21 SS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 SS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 88 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
US-10-922-651-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-877-363-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                  Š
                         61 NQKFKGRPTISVDKSKNTLYLQMNSLRAEDTAVYYCARVVYYSASYMYFDVWGQGTLVTV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 NOKPKDRFTISVDKSKNTLYLOMNSLRAEDTAVYYCARGIYFYGT-TYFDYWGQGTLVTV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EVQLVESGGGLVQPGGSLRLSCAASGYTFTSYNMHWYRQAPGKGLEWYGAIYPGNGATSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 BVQLVBSGGGLVQPGGSLRLSCAASGYSPTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: BENJUMES, MARK C.
TITLE OF INVENTION: THERAPY OF AUTOIMMUNE DISEASE IN A PATIENT WITH AN
TITLE OF INVENTION: THERAPY OF AUTOIMMUNE DISEASE IN A PATIENT WITH AN
TITLE OF INVENTION: INADEQUATE RESPONSE TO A TWP-a INHIBITOR
TILE REPERENCE: P2027R1-US
CURRENT APPLICATION NUMBER: US/10/818,765
CURRENT FILING DATE: 2004-04-06
PRIOR APPLICATION NUMBER: US 60/461,4819
PRIOR APPLICATION NUMBER: US 60/461,4819
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 2
LENGTH: 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Gaps
                                                                                                                                                                                                                                                                                                            APPLICANT: Addrew Chan
APPLICANT: Oian Gong
APPLICANT: Oian Gong
APPLICANT: Plantew Martin
TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
FILE REFERENCE: P2040RIP1
CURRENT APPLICATION NUMBER: US/11/021,874
CURRENT PILING DATE: 2004-12-22
PRIOR PILING DATE: 2004-06-04
PRIOR FILING DATE: 2003-06-06
PRIOR FILING DATE: 2003-06-06
PRIOR PILING DATE: 2003-06-06
PRIOR PILING DATE: 2003-06-05
PRIOR APPLICATION NUMBER: US 60/476,481
PRIOR APPLICATION NUMBER: US 60/476,414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 79.7%; Score 517.5; DB 6; Length 452; Best Local Similarity 82.0%; Pred. No. 3.4e-39; Matches 100; Conservative 8; Mismatches 13; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: sequence is synthesized US-11-021-874-46
                                                                                                                                                                                                                              US-11-021-874-46
i Sequence 46, Application US/11021874
i Publication No. US20050163775A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/10818765
Publication No. US20040202658A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SS 122
                                                                                                                                     121 SS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 88 121
                                                                                           120 SS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-818-765-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                          셤
                                                                                           ò
                                                                                                                       륌
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
```

```
119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 NQKPKGRPTISVDKSKNTLYLQMNSLRAEDTAVYXCARVVYYSNSYWYPDVWGQTLVTV 120
                                                                                                                                                                                                                 61 NQKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGT-TYFDYWGQGTLVTV 119
                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                              1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                            1 EVQLVESGGGLVQPGGSLRLSCAASGYTFTSYNMHWVRQAPGKGLEWVGAIYPGNGDTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EVQLVESGGGLVQPGGSLRLSCAASGYTFTSYNMHWYRQAPGKGLEWVGAIYPGNGDTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 NOKEKDRPTISVDKSKNTLYLOMNSLRAEDTAVYYCARGIYFYGT-TYFDYWGQGTLVTV
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/10877363

Publication No. US20050032130A1

GENERAL INFORMATION:

APPLICANT: BERESINI, MAUREEN

APPLICANT: SONG, AN

TITLE OF INVENTION: NEUTRALIZING ANTIBODY ASSAY AND USES THEREFOR

FILE REPERENCE: P2032R1

CURRENT APPLICATION NUMBER: US/10/877,363

CURRENT PILING DATE: 2004-06-24

PRIOR FILING DATE: 2003-07-29

NUMBER OF SEQ ID NOS: 4

SEQ ID NO 2.
                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 122;
     Length 122;
79.6%; Score 516.5; DB 4; Length 82.0%; Pred. No. 1.1e-39; ive 7; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79.6%; Score 516.5; DB 5;
82.0%; Pred. No. 1.1e-39;
tive 7; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/10922651
| Publication No. US20050053602A1
| GENERAL INFORMATION:
| APPLICANT: BRUMETTA, PAUL G.
| TITLE OF INVENTION: Therapy of Ocular Disorders
| FILE REPRENCE: P2029R1
| CURRENT APPLICATION NUMBER: US/10/922,651
| CURRENT FILING DATE: 2004-08-20
| PRIOR APPLICATION NUMBER: US 60/498,791
| PRIOR FILING DATE: 2003-08-29
| NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: Sequence is synthesized US-10-877-363-2
```

```
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 NQKFKGRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARVVYYSNSYWYFDVWGQGTLVTV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 NQKFKGRPTISVDKSKNTLYLQMNSLRAEDTAVYYCARVVYYSNSYMYFDVWGQGTLVTV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 NQKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGT-TYFDYWGQGTLVTV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 NQKFKDRFTISVDXSKNTLYLQMNSLRAEDTAVYYCARGIYFYGT-TYFDYWGQGTLVTV 119
                                                                                                                                                                                                                                                                                                                                                                                                        1 BVQLVESGGGLVQPGGSLRLSCAASGYTFTSYNMHWVRQAPGKGLEWVGAIYPGNGDTSY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                      1 EVQLVESGGGLVQPGGSLRLSCAASGYSPTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 BVQLVBSGGGLVQPGGSLRLSCAASGYTFTSYAMHWYRQAPGKGLEWYGAIYPGNGDTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVOLVESGGGLVQPGGSLRLSCAASGYSFTGHWMWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Addrew Chan
APPLICANT: Qian Gong
APPLICANT: Qian Gong
APPLICANT: Qian Gong
APPLICANT: Plavius Martin
ITILE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
FILE REFERENCE: P2040RIUS
CURRENT PAPLICATION NUMBER: US/10/861,049
CURRENT PILING DATE: 2003-06-06
PRIOR FILING DATE: 2003-06-06
PRIOR FILING DATE: 2003-06-06
PRIOR FILING DATE: 2003-06-05
PRIOR PILING DATE: 2003-06-05
PRIOR FILING DATE: 2003-06-05
                                                                                                                                                                                                                                           Query Match 79.6%; Score 516.5; DB 5; Length 122; Best Local Similarity 82.0%; Pred. No. 1.1e-39; Matches 100; Conservative 7; Mismatches 14; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 79.6%; Score 516.5; DB 5; Length Best Local Similarity 82.0%; Pred. No. 1.1e-39; Matches 100; Conservative 7; Mismatches 14; Indels
                                                                                                                                                   ) OTHER INFORMATION: Sequence is synthesized US-10-922-651-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: sequence is synthesized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-861-049-14

Sequence 14, Application US/10861049
Publication No. US20050095243A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
US-11-021-874-14
Sequence 14, Application US/11021874
Publication No. US20050163775A1
                                                           TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 SS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 88 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 SS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-861-049-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
```

```
;
TOPOLOGY: Linear
;
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-665-658-24
                                                                                                                                                                                                                                                                                                                                   US-10-665-658-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     April 13, 2006, 17:21:05; Search time 17:9651 Seconds (without alignments) 286.178 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 24,
Sequence 5, 1
                                                                                                                              US-10-727-737-17
649
1 BVQLVBSGGGLVQPGGSLRL.......PYGTTYFDYWGQGTLVTVSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 42,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 24,
Sequence 24,
Sequence 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 46,
Sequence 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 36
Sequence 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4
Sequence 1
Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence Sequence Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                         Published Applications AA New:*

1: /SIDS5/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

2: /SIDS5/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /SIDS5/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

4: /SIDS5/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

5: /SIDS5/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

7: /SIDS5/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

8: /SIDS5/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

8: /SIDS5/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-665-658-24
US-11-167-028-55
US-11-167-028-50
US-11-149-031-2
US-11-120-338-24
US-11-120-338-24
US-11-120-338-24
US-11-120-338-24
US-11-120-338-24
US-11-120-338-17
US-11-120-338-17
US-11-160-338-17
US-11-160-338-17
US-11-160-338-17
US-11-160-338-17
US-11-160-338-17
US-11-160-338-17
US-11-160-338-17
US-11-160-338-17
US-11-160-338-17
US-11-160-320-45
US-11-160-320-45
US-11-1208-422-46
US-11-208-422-46
US-11-1208-422-45
                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-11-107-028-45
US-11-107-028-46
US-11-106-820-30
                                                                                                                                                                                                                           217505 segs, 42489236 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                    protein search, using sw model
                                                                                                                                                                                                 Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                              seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query
Match 1
                                                                                                                               Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    521.5
521.5
521.5
521.5
521.5
521.5
521.5
521.5
521.5
521.5
                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                Minimum DB 8
Maximum DB 8
                                                    OM protein
                                                                                                                                                           Sequence:
                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                                                             Database
                                                                               Fun on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š.
```

```
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                     2001, 11
2002, 11
2003, 12
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
2003, 13
200
                                                                                                                                                                                                                                                                                                                                         Sequence Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
US-11-208-422-49
US-11-208-422-44
US-11-12-38-22-44
US-11-12-348-8
US-11-107-028-30
US-11-143-071-8
US-11-143-071-8
US-11-143-36-8
US-11-143-36-8
US-11-143-38-2
US-11-120-338-12
US-11-120-338-14
US-11-120-338-14
US-11-120-338-14
US-11-120-338-14
US-11-120-338-14
US-11-120-338-14
US-11-120-38-14
US-11-120-38-14
US-11-120-38-14
US-11-106-820-26
                \begin{array}{c} \mathbf{0} & \mathbf{
```

### ALIGNMENTS

```
AFFLICANT: DATULE W. FAULE W.

TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: SOUTH SAN Francisco
STATE: California
CONTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
                                                                                                                                                                                                                    NAME: Tan, Lee K.

REGISTRATION UNDERR: 39,447

REFERENCE/DOCKET NUMBER: P1014R1C1D1C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-4462

TELEPHONE: 650/225-4461

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:
Sequence 24, Application US/10665658
Publication No. US20050276801A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 121 amino acids TYPE: Amino Acid
                                               APPLICANT: Jardieu, Paula M.
```

```
61 NQKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIHPSDSETRY 60
                                                                                                                                  121 S 121
                                                                                                                                                                            121 $ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 $ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 S 121
                                                                                                                                                                                                                                                                     US-11-107-028-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                  à
                                                                            g
                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ጵ
                                                                   ô
                                                                                                                                                                                                                             61 NQKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGGGTLVTVS 120
                                                                                                                                                                                                 61 NOKPKDRFTISVDKSKATLYLOMNSLRAEDTAVYYCARGIYPYGTTYYPDYWGQGTLVTVS 120
                                                                                                                                       1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMWWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                           1 BVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                   Gaps
                                                                   ö
                       DB 6; Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 97.4%; Score 632; DB 6; Length 121; Best Local Similarity 96.7%; Pred. No. 7.3e-45; Matches 117; Conservative 1; Mismatches 3; Indels
                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/10665658
Publication No. US20050276801A1
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
             Query Match
100.0%; Score 649; DB 6.
Best Local Similarity 100.0%; Pred. No. 3e-46;
Matches 121; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/255-4462
TELEPAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 121 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94080
                                                                                                                                                                                                                                                                                       121 $ 121
                                                                                                                                                                                                                                                                                                                                    121 $ 121
                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-665-658-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-665-658-5
                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 2
                                                                                                                                                                                                                                         셤
                                                                                                                                              셤
                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                          8
```

1 BVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWANWRQAPGKGLEWVGMIAPASSSTRY

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 NQKPKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 BVQLVBSGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIHPSDSETRY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 BVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
Sequence 50, Application US/11107028
| Publication No. US20050276803A1
| GENERAL INFORMATION:
| APPLICANT: CHAN, ANDREW C. APPLICANT: GONG, QIAN
| APPLICANT: GONG, QIAN
| APPLICANT: MARTIN, FLAVIUS
| TITLE OF LINEWISHON: Method for Augmenting B Cell Depletion FILE REFERENCE: P2112R1
| CURRENT APPLICATION NUMBER: US/11/107,028
| CURRENT FILING DATE: 2005-04-15
| PRIOR PILING DATE: 2005-04-16
| WUMBER OF SEQ ID NOS: 52
| SEQ ID NO 50
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 97.4%; Score 632; DB 7; Length 121; Best Local Similarity 96.7%; Pred. No. 7.3e-45; Matches 117; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Bequence is synthesized US-11-107-028-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT

ORGANISM: Artificial sequence

PEATURE:

OTHER INFERMATION: sequence is synthesized

US-11-149-031-2
                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial sequence
```

ä

1; Gaps

Indels

DB 7; Length 122;

9

```
61 NQKFKGRPTISVDKSKONTLYLQMNSLRAEDTAVYYCARVVYYSYRYWYFDVWGQGTLVTV 120
                                                                                                                                                                                                                                                                                                                                            1 EVOLVESGGGLVQPGGSLRLSCAASGYTFTSYNMHWVRQAPGKGLEWVGAIYPGNGATSY
                                                                                                                                                                                                                                                                                                                                                                                                         61 NOKPYDRPTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYP-YGTTYFDYWGQGTLVTV
                                                                                                                                                                                                                                                                                                                     1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                             Query Match 80.4%; Score 521.5; DB 7; Best Local Similarity 82.8%; Pred. No. 6.8e-36; Matches 101; Conservative 7; Mismatches 13;
                                                                                                                                                         ) OTHER INFORMATION: sequence is synthesized US-11-120-338-24
PRIOR FILING DATE: 2004-05-05
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 24
LENGTH: 122
TYPE: PRT
ORGANISM: Artificial sequence
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 88 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 SS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-11-143-077-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
                                                                                                                                                                                                                                                                                                                     ઠ
                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Jien, Samantha
APPLICANT: Lien, Samantha
APPLICANT: Lien, Samantha
APPLICANT: Lowman, Henry B.
APPLICANT: Lowman, Henry B.
APPLICANT: Marvin, Jonathan S.
APPLICANT: Marvin, Jonathan S.
APPLICANT: Mary Yu-Ju G.
TITLE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION FILE REFERENCE: P2158R1
CURRENT APPLICATION NUMBER: US/11/208,422
CURRENT FILING DATE: 2005-08-19
PRIOR PILING DATE: 2004-08-19
PRIOR PILING DATE: 2004-08-19
NUMBER OF SEQ ID NOS: 54
IENGTH: 121
                                                                                                                                                                                                        NQKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                                                                                                                                                                                 61 NQKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 NOKFKDRPTISVDKSKNTLYLOMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 NQKFKDRFTISVDKSKGYLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                                                                  9
                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                  1 EVQLVESGGGLVQPGGSLRLSCAASGYSPTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                           EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIHPSDSETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EVOLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIHPSDSETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BVQLVESGGGLVQPGGSLRLSCAASGYSPTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                       Score 632; DB 7; Length 121;
Pred. No. 7.3e-45;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-11-120-338-24

Sequence 24, Application US/11120338

PUD11cation No. US20050271658A1

GENERAL INFORMATION:
APPLICANT: BRUNETTA, PAUL G.
APPLICANT: GREWAL, IQBAL S.
APPLICANT: WALLOCKE, PATRICIA A.
TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
FILE REFERENCE: P2079R2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 97.4%; Score 632; DB 7; Best Local Similarity 96.7%; Pred. No. 7.3e-45; Matches 117; Conservative 1; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Sequence is synthesized US-11-208-422-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/11/120,338 CURRENT FILING DATE: 2005-05-03
                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 14, Application US/11208422; Publication No. US20060067930A1; GENERAL INFORMATION:
                       97.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial sequence
                    Query Match
Best Local Similarity 96.7
Matches 117; Conservative
                                                                                                                                                                                                                                                                                              121 8 121
                                                                                                                                                                                                                                                                                                                                        121 S 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 8 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                     ķ
                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
```

```
61 NOKFKDRFTISVDKSKNTLYLOMNSLRAEDTAVYYCARGIYF-YGTTYFDYWGQGTLVTV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                           1 EVOLVESGGGLVQPGGSLRLSCAASGYTFTSYNMHWVRQAPGKGLEWVGAIYPGNGATSY
                                                                                                                                                                                                                                                                                                                                        1; Gaps
                                                                                                                                                                                                                                                                                                            Length 122;
                                                                                                                                                                                                                                                                                                                                        13; Indels
                                                                                                                                                                                                                                                                                                          DB 7;
80.4%; Score 521.5; DB 782.8%; Pred. No. 6.8e-36; tive 7; Mismatches 13
                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Sequence is synthesized US-11-143-077-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-11-143-386-24
Sequence 24, Application US/11143386
Publication No. US20060051345A1
GENERAL INFORMATION:
APPLICANT: FROHNA, PAUL A.
                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 82.8
Matches 101; Conservative
```

CURRENT FILING DATE: 2005-05-03 PRIOR APPLICATION NUMBER: US 60/568,460

```
61 NQKFKGRFTISVDKSKONTLYLQMNSLRAEDTAVYYYGARVVYYSYRYWYFDVWGQGTLVTV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 NQKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYF-YGTTYFDYWGQGTLVTV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 NOKEKORPTISVDKSKNTLYLOMNSLRAEDTAVYYCARGIYF-YGTTYFDYWGQGTLVTV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 NQKFKGRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARVVYYSYRWYFDVWGQGTLVTV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 BUQLVESGGGLVQPGGSLRLSCAASGYTFTSYNMHWVRQAPGKGLEWVGAIYPGNGATSY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EVQLVESGGGLVQPGGSLRLSCAASGYTFTSYNMHWVRQAPGKGLEWVGAIYPGNGATSY 60
                                                APPLICANT: Adams. Camellia W. APPLICANT: Adams. Camellia W. APPLICANT: Lien, Samantha APPLICANT: Lien, Samantha APPLICANT: Lien, Samantha B. APPLICANT: Meng, Yu-Ju G. TITLE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION TITLE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION CURRENT APPLICATION NUMBER: US/11/208,422 CURRENT FILING DATE: 2005-08-19 PRIOR APPLICATION NUMBER: US 60/603,057 PRIOR FILING DATE: 2004-08-19 NUMBER OF SEQ ID NOS: 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EVQLVESGGGLVQPGGSLRLSCAASGYSPTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EVOLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 80.4%; Score 521.5; DB 7; Length 451; Best Local Similarity 82.8%; Pred. No. 2e-35; Matches 101; Conservative 7; Mismatches 13; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 7; Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-11-120-338-25

Sequence 25, Application US/11120338

Sequence 25, Application US/11120338

Sequence 25, Application US/11120338

Sequence 25, Application US/11120338

APPLICANT: BRUNETTA, PAUL G.

APPLICANT: WALICKE, PATRICIA.

TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE

FILER REFERENCE: P2079R2

CURRENT APPLICATION NUMBER: US/11/120,338

CURRENT APPLICATION NUMBER: US/11/120,338

CURRENT APPLICATION NUMBER: US 60/568,460

PRIOR PILING DATE: 2004-05-05

NUMBER OF SEQ ID NOS: 25

SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 80.4%; Score 521.5; DB 7
Best Local Similarity 82.8%; Pred. No. 6.8e-36;
Matches 101; Conservative 7; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , OTHER INFORMATION: sequence is synthesized US-11-208-422-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: sequence is synthesized US-11-120-338-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial sequence
            No. US20060067930A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial sequence
                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 SS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 SS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઢ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 NOKPKORPTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYF-YGTTYPDYWGQGTLVTV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 NQKFKGRPTISVDKSKNTLYLQMNSLRAEDTAVYYCARVVYYSYRYWYPDVWGQGTLVTV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 NQKFKGRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARVVYYSYRYHYFDVWGQGTLVTV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 NOKFKDRPTISVDKSKNTLYLOMNSLRAEDTAVYYCARGIYF-YGTTYFDYWGQGTLVTV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 BUQLVESGGGLVQPGGSLRLSCAASGYTFTSYNMHWVRQAPGKGLEWVGAIYPGNGATSY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVQLVESGGGLVQPGGSLRLSCAASGYTFTSYNMHWYRQAPGKGLEWVGAIYPGNGATSY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

80.4%; Score 521.5; DB 7; Length 122;
Best Local Similarity 82.8%; Pred. No. 6.8e-36;
Matches 101; Conservative 7; Mismatches 13; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 80.4%; Score 521.5; DB 7; Length 122; Best Local Similarity 82.8%; Pred. No. 6.8e-36; Matches 101; Conservative 7; Mismatches 13; Indels 1
TITLE OF INVENTION: METHOD FOR TREATING MULTIPLE SCLEROSIS FILE REFERENCE: P2134R1
CURRENT APPLICATION NUMBER: US/11/143,386
CURRENT FILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US 60/576,993
PRIOR PILING DATE: 2004-06-04
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hitrays, Elena
TITLE OF INVENTION: METHOD FOR TREATING SJOGREN'S SYNDROME
FILE REFERENCE: P2149R1
CURRENT APPLICATION NUMBER: US/11/187,364
CURRENT FILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: US 60/590,302
PRIOR PILING DATE: 2004-07-22
NUMBER OF SEQ ID NOS: 36
LENGTH: 122
                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Sequence is synthesized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Sequence is synthesized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BSULT 10
S-11-208-422-45
Sequence 45, Application US/11208422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-11-187-364-36
, Sequence 36, Application US/11187364
, Publication No. US20060062787A1
, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 SS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 SS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 $$ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 SS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-11-187-364-36
                                                                                                                                                                                                                                                                                                                                                                                             US-11-143-386-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
```

Gaps

1;

셤

ò g

셤 δ

ò

1,

1; Gaps

```
61 NQKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYF-YGTTYFDYWGQGTLVTV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 NOKFKGRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARVVYYSYRYWYPDVWGQGTLVTV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
1 EVQLVESGGGLVQPGGSLRLSCAASGYTPTSYNMHWVRQAPGKGLEWVGAIYPGNGATSY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EVQLVESGGGLVQPGGSLRLSCAASGYTFTSYNMHWYRQAPGKGLEWVGAIYPGNGATSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 521.5; DB 7; Length 451;
Pred. No. 2e-35;
7; Mismatches 13; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80.4%; Score 521.5; DB 7; Length 452;
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hitraya, Rlena
TITLE OF INVENTION: METHOD FOR TREATING SJOGREN'S SYNDROWE
FILE REFERENCE: P2149R1
CURRENT APPLICATION NUMBER: US/11/187,364
CURRENT APPLICATION NUMBER: US 60/590,302
PRIOR APPLICATION NUMBER: US 60/590,302
PRIOR PILING DATE: 2004-07-22
PRIOR PILING DATE: 2004-07-22
NUMBER OF SEQ ID NOS: 36
SEQ ID NO 34
LENGTH: 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17. Application US/11120338
Publication No. US20050271658A1
GENERAL INFORMATION:
APPLICANT: BRUNETTA, PAUL G.
APPLICANT: GREWAL, IQBAL S.
APPLICANT: GREWAL, IQBAL S.
TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
CURRENT APPLICATION NUMBER: US/11/120,338
CURRENT PILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: US 60/568,460
PRIOR FILING DATE: 2004-05-05
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 17.
LENGTH: 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-11-187-364-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: sequence is synthesized
                                                                                                                                                                                                                                                                                                           Sequence 34, Application US/11187364
Publication No. US20060062787A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80.4%;
82.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 82.8<sup>1</sup>
Matches 101; Conservative
                                                                                                                                              120 88 121
                                                                                                                                                                                       121 SS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 SS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
US-11-120-338-17
                                                                                                                                                                                                                                                                                     US-11-187-364-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-11-120-338-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                   셤
                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 NQKFXDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYF-YGTTYFDYWGQGTLVTV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 NQKFKGRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARVVYYSYRYWYFDVWGQGTLVTV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EVQLVESGGGLVQPGGSLRLSCAASGYTFTSYNMHWVRQAPGKGLEWVGAIYPGNGATSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 80.4%; Score 521.5; DB 7; Length 451; Best Local Similarity 82.8%; Pred. No. 2e-35; Matches 101; Conservative 7; Mismatches 13; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-11-143-386-25
Sequence 25, Application US/11143386
Sequence 25, Application US/11143386
Sequence 25, Application US/11143386
Sequence 25, Application US/11143386
SPLICANT: FROHNA, PAUL A.
TITLE OF INVENTION: METHOD FOR TREATING MULTIPLE SCLEROSIS FILE REPRENCE: P2134R1
CURRENT APPLICATION NUMBER: US/11/143,386
CURRENT FILING DATE: 2005-06-02
PRIOR PILING DATE: 2005-06-04
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 25
LENGTH: 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 521.5; DB 7;
Pred. No. 2e-35;
7; Mismatches 13;
                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Brunetta, Paul G.
TITLE OF INVEXTION: METHOD FOR TREATING LUPUS
TITLE REPERENCE: P2131811
CURRENT APPLICATION NUMBER: US/11/143,077
CURRENT PILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US 60/577,235
PRIOR APPLICATION NUMBER: US 60/617,997
PRIOR APPLICATION NUMBER: US 60/617,997
PRIOR PILING DATE: 2004-06-04
PRIOR PILING DATE: 2004-10-11
NUMBER OP SEQ ID NOS: 24
LENGTH: 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , OTHER INFORMATION: Sequence is synthesized.
US-11-143-386-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FEATURE:
, OTHER INPORMATION: Sequence is synthesized
US-11-143-077-22
                                                                                                                                                                                          Sequence 22, Application US/11143077
Publication No. US20060024295A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 82.8
Matches 101; Conservative
                                                                         SS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SS 122
                             SS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 SS 121
                                                                                                                                                                      S-11-143-077-22
                             120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
                                                                         121
```

ā

윰 ፘ

ð

g

ઠે

PEATURE:

```
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
TELECOMMUXICATION INFORMATION:
TELEPHONE: 650/225-4462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | TELERPAX: 650/225-4462
| TELERPAX: 650/922-9881
| SEQUENCE CHRACTERISTICS:
| SEQUENCE CHRACTERISTICS:
| TYPE: Amino Acid
| TYPE: Amino Acid
| SEQUENCE DESCRIPTION: SEQ ID NO: 2:
| US-10-665-658-2
                                                                                                                                                              April 13, 2006, 17:21:05; Search time 16.0349 Seconds (without alignments) 286.178 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, A Sequence 5, A Sequence 77, A Seque
                                                                                                                                                                                                                                                                           US-10-727-737-2
560
1 DIQMIQSPSSLSASVGDRVT......QQHNEYPLTFGQGTKVBIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15,
Sequence 49,
Sequence 1,
Sequence 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2,
Sequence 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published Applications AA New:*

1: /SIDSS/ptodata/1/pubpaa/US06 NEW PUB.pep:*

2: /SIDSS/ptodata/1/pubpaa/US06 NEW PUB.pep:*

3: /SIDSS/ptodata/1/pubpaa/US07 NEW PUB.pep:*

4: /SIDSS/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

5: /SIDSS/ptodata/1/pubpaa/US09 NEW_PUB.pep:*

6: /SIDSS/ptodata/1/pubpaa/US10 NEW_PUB.pep:*

7: /SIDSS/ptodata/1/pubpaa/US11 NEW_PUB.pep:*

8: /SIDSS/ptodata/1/pubpaa/US11 NEW_PUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-11-143-386-3
US-11-187-364-3
US-10-981-356A-5
US-11-096-046-5
US-11-154-337-5
US-11-182-908-5
US-11-102-120-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-771-257-77
US-11-127-677-75
US-11-051-453-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217505 segs, 42489236 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            $
Query
Match Length D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database
                                                                                                                                                                      Run on:
```

Sequence 16, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 17, Appl Sequence 700, Appl Sequence 700, Appl Sequence 724, Appl Sequence 13, Appl Sequence 13, Appl Sequence 3, Appli Sequence 6, Appli	odies
US-11-051-453-46 US-11-127-932-14 US-11-127-932-18 US-11-127-903-14 US-11-127-903-14 US-11-08-34-397-14 US-11-09-739-714 US-11-199-739-700 US-11-199-739-700 US-11-199-739-724 US-11-041-095-13 US-11-041-095-13 US-11-051-453-30 US-11-025-366A-6 US-11-102-512-6 US-11-102-512-6 US-11-098-758-6 US-11-098-758-6	nus/1066568  nus/1066568  itieu, Paula M.  itieu, Paula M.  itieu, Paula M.  itieu, Paula M.  itieu, Leonard G.  ITON: Humanized Anti-CD11a Antibodies  ADDRESS:  i Genentech, Inc.  BDA Way  h San Francisco  Lifornia  BE 3.5 inch, 1.44 Mb floppy disk  IEM PC compatible  SYSTEM: PC-DOS/MS-DOS  WINDERT: US/10/665,658  TES 19-SEP-2003  ATION DATA:  NN NUMBER: 08/974899  FE: 27-NOV-1996  NN NUMBER: 08/97499  FE: 20-NOV-1996  NN NUMBER: 09/420745  FE: 20-NOV-1999  NN NUMBER: 09/420745  FE: 20-NOV-1999  NN NUMBER: 09/975798
88.6 88.4 88.4 109 7 88.4 109 7 88.4 109 7 88.0 108 6 87.9 214 7 87.9 214 7 87.9 87.7 234 7 87.7 234 7 87.7 87.7 87.7 87.5 108 6 87.5 108 6 87.5 108 7 87.5 108 7 108	pplicatio o. US2005 Oo. US2005 Oo
26 27 27 29 29 30 30 30 30 30 30 30 40 40 40 40 40 40 40 40 40 40 40 40 40	RESULT 1 US-10-65-658-2 Sequence 2, Appli Publication No. U GENERAL INFORMA APPLICANT: TITLE OF I NUMBER OF CORRESPOND STREES STATE COUNTIER R MEDIU COMPU COMPU COMPU COMPU STATE S

Length 214;

```
Query Match
Best Local Similarity 100.0%; Pred. No. 5.9e-39;
Matches 108; Conservative 0; Mismatches 0;
                     , OTHER INFORMATION: Sequence is synthesized US-11-208-422-15
                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
US-11-107-028-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-11-107-028-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-11-149-031-1
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Adams, Camellia W.
APPLICANT: Lien, Samantha
APPLICANT: Lowman, Henry B.
APPLICANT: Lowman, Henry B.
APPLICANT: Lowman, Henry B.
APPLICANT: Meng, Yu-Ju G.
APPLICANT: Meng, Yu-Ju G.
TITLE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION
FILE REFERENCE: P2158N1
CURRENT APPLICATION NUMBER: US/11/208,422
CURRENT APPLICATION NUMBER: US 60/603,057
PRIOR APPLICATION NUMBER: US 60/603,057
NUMBER OF SEQ ID NOS: 54
SEQ ID NO 3
SEQ ID NO 3: 54
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Adams, Camellia W.
APPLICANT: Lien, Samantha
APPLICANT: Lowman, Henry B.
APPLICANT: Lowman, Henry B.
APPLICANT: Meng, Yu-Ju G.
APPLICANT: Meng, Yu-Ju G.
TITLE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION
FILE REFERENCE: P2158R1
CURRENT APPLICATION NUMBER: US/11/208,422
CURRENT APPLICATION NUMBER: US 60/603,057
PRIOR PILING DATE: 2004-08-19
NUMBER OF SEQ ID NOS: 54
NUMBER OF SEQ ID NOS: 54
LENGTH: 214
                                                                                                                                                           1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIQMIQSPSSLSASVGDRVIITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS 60
                                                                                                                       1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gapa
                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                  61 RPSGSGSGTDFTLTISSLQPEDFATYYCQQHNBYPLTFGGGTKVEIKR 108
                                                                                                                                                                                                                               61 RPSGSGSGTDFTLTISSLQPEDPATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNBYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGGGTKVEIKR 108
                   Query Match
100.0%; Score 560; DB 6; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.2e-39;
Matches 108; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 560; DB 7; Length 108; Best Local Similarity 100.0%; Pred. No. 3.2e-39; Matches 108; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) OTHER INFORMATION: Sequence is synthesized US-11-208-422-13
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13, Application US/11208422
Publication No. US20060067930A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15, Application US/11208422
Publication No. US20060067930A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
US-11-208-422-15
                                                                                                                                                                                                                                                                                                                                                                                          -11-208-422-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

```
ö
                                                                                                 1 DIQMIQSPSSLSASVGDRVIITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS 60
                                                           1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: GOFE, BERNARD S.

TITLE OF INVENTION: Method of Treating Granuloma Annulare or Sarcoid
FILE REFERENCE: P2129R1
CURRENT APPLICATION NUMBER: US/11/149,031
PRIOR APPLICATION NUMBER: US 60/578,768
PRIOR FILING DATE: 2004-06-09
PRIOR FILING DATE: 2004-06-09
PRIOR FILING DATE: 2004-06-09
PRIOR FILING DATE: 2004-06-10
RIOR FILING DATE: 2004-06-10
   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                61 RFSGSGSGTDFTLTISSLQPEDPATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                61 RPSGSGSGTDFTLTISSLQPEDFATYYCQQHNBYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: CHAN, ANDREW C.
APPLICANT: GNG, OLAN
APPLICANT: GONG, OLAN
APPLICANT: MARTIN, FLAVIUS
TITLE CANT: MARTIN, FLAVIUS
FILE REFERENCE: P2112R1
CURRENT APPLICATION NUMBER: US/11/107,028
CURRENT FILING DATE: 2005-04-15
FRIOR FILING DATE: 2004-04-16
NUMBER OF SRQ ID NOS: 52
SRQ ID NO 49
LENGTH: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RPSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 RFSGSGSGTDFTLTISSLOPEDFATYYCOONNEYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 107;
0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 99.1%; Score 555; DB 7; 1
Best Local Similarity 100.0%; Pred. No. 8.1e-39;
Matches 107; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: sequence is synthesized
                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 49, Application US/11107028
; Publication No. US20050276803A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 1, Application US/11149031; Publication No. US20060013818A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Artificial sequence
```

```
1 Similarity 89.8 97; Conservative
                                                                                                                                   JS-11-120-338-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-11-143-077-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 요
  ठ
                                   ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                 1 DIQMIQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIQMIQSPSSLSASVGDRVIITCRASQSISNYLAWYQQKPGKAPKLLIYAASSLESGVPS 60
                                                                                                                                                           1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIOMTOSPSSLSASVGDRVTITCRASKTISKYLAWYQOKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                    61 RPSGSGSGTDPTLTISSLQPEDFATYYCQQHNRYPLTFGQGTKVBIK 107
                                                                                                                                                                                                                                                                            61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNBYPLTFGQGTKVBIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

90.4%; Score 506; DB 6; Length 108;
Best Local Similarity 89.8%; Pred. No. 7.9e-35;
Matches 97; Conservative 6; Mismatches 5; Indels
                                                                Length 107;
                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Jardieu, Paula M.
Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

COMPUTER: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 11M PC compatible COMPUTER: 11M PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/665,658

FILING DATE: 19-Sep-2003

CLASSIFICATION NUMBER: 60/031971

FILING DATE: 27-NOV-1996

APPLICATION NUMBER: 60/91977

APPLICATION NUMBER: 09/42075

FILING DATE: 20-NOV-1997

APPLICATION NUMBER: 09/420745

FILING DATE: 20-OCT-1999

APPLICATION NUMBER: 09/42075

FILING DATE: 28-FEB-2001

ATYORNEY/AGRY INFORMATION:

ATYORNEY/AGRY INFORMATION:
                                                                Query Match 99.1%; Score 555; DB 7; I
Best Local Similarity 100.0%; Pred. No. 8.1e-39;
Matches 107; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
TELECOMMUNICATION INFORMATION:
; OTHER INFORMATION: sequence is synthesized
US-11-149-031-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/10665658
Publication No. US20050276801A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 108 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Tan, Lee K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
US-10-665-658-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-665-658-3
                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                             셤
```

```
1 DIQMIQSPSSLSASVGDRVIITCRASQSISNYLAWYQQKRGKAPKLLIYAASSLESGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIOMIQSPSSISASVGDRVIIICRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLAWYQQKPGKAPKLLIYAASSLBSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIOMTOSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
61 RESGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                          61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSLPWTFGQGTKVBIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RFSGSGSGTDFTLTISSLOPEDFATYYCOOYNSLPWTFGGGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Indels
                                                                                                                                                         Sequence 3, Application US/11120338
; Publication No. US20050271658A1
; Publication No. US20050271658A1
; GENERAL INFORMATION:
    APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: GREWAL, IQBAL S.
; APPLICANT: WALICKE, PATRICIA A.
; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
; TITLE OF INVENTION NUMBER: US/11/120,338
; CURRENT PILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: US 60/568,460
; PRIOR FILING DATE: 2004-05-05
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 3
; SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 506; DB 7;
Pred. No. 7.9e-35;
6; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/11143077
PUDLICATION NO. US20060024295A1
GENERAL INFORMATION:
APPLICANT: Brunetta, Paul G.
TITLE OF INVENTION: METHOD FOR TREATING LUPUS
FILE REFERENCE: P2133R1
CURRENT APPLICATION NUMBER: US/11/143,077
CURRENT FILING DATE: 2005-06-02
PRIOR FILING DATE: 2004-06-04
PRIOR FILING DATE: 2004-06-1
PRIOR FILING DATE: 2004-10-11
PRIOR FILING DATE: 2004-10-11
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 506; DB 7;
Pred. No. 7.9e-35;
6; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: sequence is synthesized US-11-120-338-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Sequence is synthesized US-11-143-077-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.4%;
I Similarity 89.8%;
97; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial sequence
```

ö

```
1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-187-364-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-11-187-364-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIQMIQSPSSLSASVGDRVTITCRASQSISNYLAWYQQKPGKAPKLLIYAASSLBSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gape
                                                                                          RESULT 9
US-11-190-364-3
i Sequence 3, Application US/11190364
i Publication No. US20060024300A1
i GENERAL INPORMATION:
I TILE OF INVENTION: Immunoglobulin Variants and Uses Thereof
FILE REPERENCE: P1990R3C1P1
i CURRENT PILING DATE: 2005-07-26
FRIOR APPLICATION NUMBER: US/11/190,364
CURRENT PILING DATE: 2005-12-16
i PRIOR APPLICATION NUMBER: US 60/434,115
i PRIOR PILING DATE: 2003-12-01
i PRIOR PILING DATE: 2003-12-06
i PRIOR PILING DATE: 2003-12-16
i PRIOR PILING DATE: 2005-06-07
i NUMBER OF SEQ ID NOS: 38
i EBNOTH: 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fublication No. US20060034835A1
Fublication No. US20060034835A1
Fublication No. US20060034835A1
GENERAL INFORMATION:
APPLICANT: Adams ET AL.
TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof
FILE REPRENCES: 1990R3C1
CURRENT APPLICATION NUMBER: US 60/434,115
PRIOR APPLICATION NUMBER: US 60/434,115
PRIOR PRILING DATE: 2002-12-01
PRIOR APPLICATION NUMBER: US 60/526,163
PRIOR APPLICATION NUMBER: US 60/526,163
PRIOR APPLICATION NUMBER: PCT/US03/40426
PRIOR APPLICATION NUMBER: PCT/US03/40426
PRIOR FILING DATE: 2003-12-01
PRIOR FILING DATE: 2003-12-16
SRO ID NO 3
LENGTH: 108
61 RFSGSGSGTDFTLTISSLQPEDPATYYCQQHNBYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 90.4%; Score 506; DB 7; Length 108; Best Local Similarity 89.8%; Pred. No. 7.9e-35; Matches 97; Conservative 6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

90.4%; Score 506; DB 7;
Best Local Similarity 89.8%; Pred. No. 7.9e-35;
Matches 97; Conservative 6; Mismatches 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
FRATURE:
OTHER INFORMATION: Sequence is synthesized
US-11-147-780-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Sequence is synthesized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -11-147-780-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-11-190-364-3
                         윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
1 DIQMIQSPSSLSASVGDRVIITCRASQSISNYLAWYQQKPGKAPKLLIYAASSLESGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DIQMIQSPSSLSASVGDRVTITCRASQSISNYLAWYQQKPGKAPKLLIYAASSLESGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIOMIOSPSSLSASVGDRVIITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIQMIQSPSSLSASVGDRVIITCRASQSISNYLAWYQQKPGKAPKLLIYAASSLBSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIOMIQSPSSLSASVGDRVIITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSLPWTFGQGTKVEIKR 108
                                                                                                                       61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSLPWTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSLPWTFGQGTKVEIKR 108
                                                                                    61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RPSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                               Sequence 3, Application US/11143386;
Publication No. US20060051345A1
GENERAL INFORMATION:
APPLICANT: FROHNA, PAUL A.
TITLE OF INVENTION: METHOD FOR TREATING MULTIPLE SCIEROSIS
FILE REFERENCE: P2134R1
CURRENT APPLICATION NUMBER: US/11/143,386
CURRENT FILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US 60/576,993
PRIOR APPLICATION NUMBER: US 60/576,993
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/11187364
; Publication No. US20060062787A1
; GENERAL INFORMATION:
; APPLICANT: Hitraya, Elena
; TITLE OF INVENTION: METHOD FOR TREATING SJOGREN'S SYNDROME
; FILE REFERENCE: P2149R1
; CURRENT APPLICATION NUMBER: US/11/187,364
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US 60/590,302
; PRIOR FILING DATE: 2004-07-22
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
90.4%; Score 506; DB 7; Length 108;
Best Local Similarity 89.8%; Pred. No. 7.9e-35;
Matches 97; Conservative 6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 90.4%; Score 506; DB 7; Local Similarity 89.8%; Pred. No. 7.9e-35; nes 97; Conservative 6; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           p FEATURE:
p OTHER INFORMATION: Sequence is synthesized.
US-11-143-386-3
```

```
Search completed: April 13, 2006, 17:25:18 Job time: 17:0349 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 89.7%;
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 5
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIQMIQSPSSLSASVGDRVIITCRASQSISNYLAWYQQKPGKAPKLLIYAASSLESGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLAWYQQKPGKAPKLLIYAASSLESGVPS 60
                                                       Sequence 5. Application US/10981356A

Publication No. US20060015952A1

Fabrication No. US20060015952A1

Fabrication No. US20060015952A1

FILE OF INVENTION:

TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT

FILE REPERENCE: 192668A1

FURRENT PAPLICATION NUMBER: US/10/981,356A

CURRENT PILING DATE: 2004-11-04

PRIOR PLILING DATE: 2004-11-13

PRIOR PLILING DATE: 2004-31-11-13

PRIOR APPLICATION NUMBER: US 60/557,951

PRIOR PLILING DATE: 2004-03-31

NUMBER OF SEQ ID NOS: 45

LENGTH: 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RFSGSGSGTDFTLTISSLOPEDPATYYCQQYNSLPWTFGQCTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 90.4%; Score 506; DB 6; Length 109; Best Local Similarity 89.8%; Pred. No. 8e-35; Matches 97; Conservative 6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 7; Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5. Application US/11096046

Publication No. US20050276802A1

GENERAL INFORMATION:
APPLICANT: ADAMS, CAMELLIA W.
APPLICANT: FILVAROFF, ELLEN H.
APPLICANT: PRESTRA, LEGONAG
APPLICANT: PRESTRA, LEGONAG
APPLICANT: PRESTRA, LEGONARD G.
APPLICANT: PRESTRA, LEGONARD G.
APPLICANT: PRESTRA, LEGONARD G.
TITLE OF INVENTY PRESTRA.
FILE REFERENCE: P1954R1US
CURRENT APPLICATION NUMBER: US/11/096,046
CURRENT APPLICATION AND RESTRANCE
CURRENT APPLICATION NUMBER: US/11/096,046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 90.4%; Score 506; DB 7, Best Local Similarity 89.8%; Pred. No. 8e-35; Matches 97; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: sequence is synthesized US-11-096-046-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTHER INFORMATION: Sequence is synthesized U3-10-981-356A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US/11/096,00-
PRIOR APPLICATION NUMBER: US 60/558,290
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 5
TENGTH: 109
                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial sequence
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial sequence
                    RESULT 13
|US-10-981-356A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EESULT 14
US-11-096-046-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>립</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ક
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ሯ
```

61 RPSGSGSGTDPTLTISSLQPEDPATYYCQQHNEYPLTPGQGTKVEIKR 108

а ò

```
1 DIQMIQSPSSLSASVGDRVIITCRASQSISNYLAWYQQKPGKAPKLLIYAASSLSSCVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSLPWTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVBIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSLPWTFGQGTKVBIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 501; DB 7; Length 107; Pred. No. 2e-34; 6; Mismatches 5; Indels
                                                                                                                                                         Sequence 5, Application US/11154337
Publication No. US20060013819A1
GENERAL INPORMATION:
ITLE OF INVENTION: THERAPY OF PLATINUM-RESISTANT CANCER
FILE REPREMENCE: P2146R1
CURRENT APPLICATION NUMBER: US/11/154,337
CURRENT FILING DATE: 2005-06-15
PRIOR PILING DATE: 2006-06-16
NUMBER: OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: sequence is synthesized US-11-154-337-5
```

## THIS PAGE IS BLANK

Sequence Sequence Sequence

Sequence

Sequence Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence

Sequence

us-10-727-737-2.rapbm

Title: Perfect score:

Run on:

Sequence

Scoring table:

Searched:

Database

Result

Š

```
DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 560; DB 3; Length 108; 100.0%; Pred. No. 4e-39; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDER: 24
CORRESPONDER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/795,798 FILING DATE: 28-Peb-2001 CLASSIFICATION: <Unknown>
US-10-125-687-8

US-10-996-191-8

US-10-725-962-36

US-10-725-962-36

US-10-800-525-36

US-10-800-525-30

US-10-625-105-30

US-10-625-105-30

US-10-469-125-8

US-10-469-125-8

US-10-910-911-20

US-10-910-911-44

US-10-910-911-44

US-10-920-144-6

US-10-920-144-6
                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 40,378
REFERENCE/DOCKEY NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
PRIOR APPLICATION WUBBR: 08/974,899
FILING DATE: <UNKNOWN-)
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09795798
Publication No. US20030207336A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 108 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Lee, Wendy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 108; Conservative
    US-09-795-798-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-795-798-2
      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Appli
Appli
Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Appl
Appl
Appli
Appli
Appli
Appli
Appli
Appli
                                                                                                                                     April 13, 2006, 17:19:49; Search time 106.114 Seconds (without alignments) 425.257 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 47, R
Sequence 12, R
Sequence 3, Ag
                                                                                                                                                                                                                                                           1 DIQMTQSPSSLSASVGDRVT.....QHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2,
Sequence 5,
Sequence 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence Sequence Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Published Applications AA Main: * cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep: * cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep: * cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep: * cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep: * cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep: * cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep: * cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep: * cgn2_6/ptodata/1/pubpaa/US11_P
                        GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-861-049-38
US-10-974-591-12
US-11-021-874-38
US-09-811-123-6
US-09-819-13-6
US-09-809-739-10
US-10-62-061-10
US-10-404-724-68
US-10-835-641-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-056-160B-12
US-09-795-798-3
                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                        1867569 segs, 417829326 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                  US-10-727-737-2
560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query
Match Length
```

ö 9 9

Gaps

```
TITLE OF INVENTION: REDUCING PROTEIN A LEACHING DURING PROTEIN A AFFINITY CHROMATOGRAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-726-258-47
                                                                                                                                                                                                                                                                                                        US-10-877-532-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JS-10-423-299-3
                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                        RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNBYPLTFGQGTKVBIKR 108
                                                  61 RFSGSGSGTDFTLTISSLOPEDFATYYCQQHNEYPLTFGGGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RPSGSGSGTDFTLTISSLQPEDPATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 560; DB 4; Length 108; Best Local Similarity 100.0%; Pred. No. 4e-39; Matches 108; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WINPAtin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA.

APPLICATION NUMBER: US/10/727,737

FILING DATE: 03-Dec-2003

CLASSIPICATION: «Unknown»

PRIOR APPLICATION NUMBER: US/08/975,329B

FILING DATE: 20-NOV-1997

APPLICATION NUMBER: 60/031945

FILING DATE: 27-NOV-1996

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                  APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Antibody Mutants
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STRERT: I DNA May
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1064R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPRONE: 650/255-1994
TELEPRAK: 650/525-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 antho acids
TYPE: Antho Acid
                                                                                                                                                                                 Sequence 2, Application US/10727737 Publication No. US20040146507A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/10877532
Publication No. US20050038231A1
GENERAL INFORMATION:
APPLICANT: FAHRNER, ROBERT L.
APPLICANT: LAVERDIERE, AMY
APPLICANT: MCDONALD, PAUL J.
APPLICANT: O'LEARY, RHONA M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Lee, Wendy M.
                                                                                                                                                             JS-10-727-737-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-727-737-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-877-532-5
                        61
                        8
                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNBYPLTFGQGTKVBIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RFSGSGSGTDFTLTISSLQPEDFATYYCQOHNEYPLTFGGGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 560; DB 5; Length 108; 100.0%; Pred. No. 4e-39; Length 108; tive 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: FOLLMAN, DEBORAH
APPLICANT: LEBRETON, BENEDICTE
APPLICANT: LEBRETON, BENEDICTE
APPLICANT: LEBRETON, BENEDICTE
TITLE OF INVANTION: NON-APPLINITY PURIFICATION OF PROTEINS
FILE REPREBENCE: 39766-0121A
CURRENT FILING DATE: 2003-04-25
PRIOR APPLICATION NUMBER: US 60/375,953
PRIOR APPLICATION NUMBER: US 60/375,953
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 560; DB 4;
Best Local Similarity 100.0%; Pred. No. 7.8e-39;
Matches 108; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 47, Application US/09726258
Publication No. US20030021790A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Heei, Vanessa
APPLICANT: Koumenis, Iphigenia
APPLICANT: Leong, Steven R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: sequence is synthesized
FILE REPERENCE: P2015R1
CURRENT APPLICATION NUMBER: US/10/877,532
CURRENT FILING DATE: 2004-06-24
PRIOR APPLICATION NUMBER: US 60/490,500
PRIOR FILING DATE: 2003-07-28
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/10423299; Publication No. US20030229212A1; GENERAL INFORMATION:
                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 108; Conservative
```

```
Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-056-160B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-795-798-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DIOMTOSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYYSGSTLESGVP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DIOMIQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLI-YSGSTLQSGVP
APPLICANT: Presta, Leonard G.
APPLICANT: Shahrokh, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSE: Genenter' STREET STRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 SRPSGSGSGTDFTLTISSLQPEDPATYYCQQHNBYPLTFGGGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SRPSGSGSGTDFTLTISSLOPEDFATYYCQQHNEYPLTFGQGTKVEIKR 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 97.6%; Score 546.5; DB 3; Length 109; Best Local Similarity 98.2%; Pred. No. 5.4e-38; Matches 107; Conservative 1; Mismatches 0; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genetech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/726,258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Application US/09056160B
Fatent No. US2002032315A1
GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Presta, Leonard G.
APPLICANT: Cowman, Henry B.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DAM Way
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIPLICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 09/234,182
FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 60/094003
APPLICATION NUMBER: 24-JUL-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 91085R4-1A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARCTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ropology: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS-09-056-160B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-726-258-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
```

```
1 DIQMIQSPSSLSASVGDRVITTCRASQSISNYLAWYQQKPGKAPKLLIYAASSLESGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEB: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible CORRUTER: IBM PC compatible CORRUTER: IBM PC compatible COPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winbatin (Genentech) CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/795,798 FILING DATE: SB-Feb-2001 CLASSIFICATION AUMBER: 08/974,899 FILING DATE: «UNKnown»

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: 08/974,899 FILING DATE: «UNKnown»

ATTORNEY/AGENT INPORMATION:

NAME: Lee, Wendy M. REGISTRATION NUMBER: 40,378

REGISTRATION NUMBER: 91014R1

TELECOMMUNICATION INPORMATION:
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/09/056,160B FILING DATE: 06-Apr-1998 CLASSIFICATION NUMBER: 60/054,856 FILING DATE: 06-AGG-1997 ATORNEY-AGGNT INPORMATION: NAME: HABAK, JANEL E. REGISTRATION NUMBER: 28,616 REGISTRATION NUMBER: 28,616 REGISTRATION NUMBER: 28,616 REGISTRATION NUMBER: 189,616 REFERENCE/DOCKET NUMBER: PLOSSIE TELECOMMUNICATION INPORMATION: TELEBRUNE: 650/225-1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.4%; Score 506; DB 3;
89.8%; Pred. No. 1.2e-34;
tive 6; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09795798
Publication No. US200310207336A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 89.8
Matches 97; Conservative
```

```
RESULT 10
US-10-861-049-38
                                                                                                                                                                                                                                                                                                US-10-727-737-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-727-737-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                         g
                                                                                                                                                                  ò
                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                     1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLAWYQQKPGKAPKLLIYAASSLBSGVPS 60
                                                                                                                                                                                                                                                                                            1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                      RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSLPWTFGQGTKVBIKR 108
                                                                                                                                                                                                         Length 108;
                                                                                                                                                                                                                                                   Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPER 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winsatin (Genentech)
                                                                                                                                                                                                         Score 506; DB 3;
Pred. No. 1.2e-34;
6; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093R2C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,10/234,671
FILING DATE: 03-Sep-2002
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 09/056160
FILING DATE: 06-APR-1998
APPLICATION NUMBER: 60/126446
FILING DATE: 07-APR-1997
APPLICATION NUMBER: 60/054856
FILING DATE: 06-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: Linear SEQ ID NO: 12: US-10-234-671-12
                                                                                                                       TOPOLOGY: Linear SEQUENCE DESCRIPTION: SEQUENCE DESCRIPTION: SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Genentech, Inc. STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12, Application US/10234671
Publication No. US20030190317A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
                   INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 108 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION: NAME: Cui, Steven X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 650/952-9881
MATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                         Query Match
Best Local Similarity 89.8%;
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-234-671-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION
                                                                                                                                                                US-09-795-798-3
                                                                                                                                                                                                                                                                                                                                     윱
                                                                                                                                                                                                                                                                                                                                                                              ઠ
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                           1 DIQMIQSPSSLSASVGDRVIITCRASQSISNYLAWYQQKPGKAPKLLIYAASSLESGVPS 60
                                                                                                 1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIQMIQSPSSLSASVGDRVTITCRASQSISNYLAWYQQKPGRAPKLLIYAASSLESGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                   Gaps
                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSLPWTFGQGTKVBIKR 108
                                                                                                                                                                                                   61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSLPWTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90.4%; Score 506; DB 4; Length 108; 89.8%; Pred. No. 1.2e-34; rive 6; Mismatches 5; Indels
Score 506; DB 4; Length 108;
Pred. No. 1.2e-34;
6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: Inh PC compatable OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/727,737
FILING DATE: 03-Dec-2003
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/975,329B
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 60/031945
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1064R1
TELECOMMUNICATION INPORMATION:
TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/10727737
Publication No. US20040146507A1
GENERAL INFORMATION:
APPLICANT: Prests, Leonard G.
ATITLE OF INVENTION: Antibody Mutants
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ 1D NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
Query Match
Best Local Similarity 89.8%;
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94080
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 89.8
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Lee,
```

```
REGISTRATION NUMBER: 44,637
PEPPERNCK/DOCKET NUMBER: P1093P1D1C1
                                            REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 90.4%;
Best Local Similarity 89.8%;
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 90.4%;
Best Local Similarity 89.8%;
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Sharon Erickson APPLICANT: Ralph Schwall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-874-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIQMIQSPSSLSASVGDRVIIITCRASKIISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIQMIQSPSSLSASVGDRVITITCRASQSISNYLAWYQQKPGKAPKLLIYAASSLESGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                         ### PRIOR APPLICATION NO. USZUGOGOSZASAL

### PEDITCANT: Andrew Chan

### APPLICANT: Andrew Chan

### APPLICANT: Andrew Chan

### APPLICANT: Plavius Martin

### TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS

### TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS

### TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS

### CURRENT APPLICATION NUMBER: US 60/476,531

### PRIOR PILING DATE: 2003-06-06

### PRIOR APPLICATION NUMBER: US 60/476,414

### PRIOR PILING DATE: 2003-06-05

### PRIOR PILING DATE: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSLPWTFGQGTKVBIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 5; Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genethech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/974,591
FILING DATE: 26-Oct-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 90.4%; Score 506; DB 5; Best Local Similarity 89.8%; Pred. No. 1.2e-34; Matches 97; Conservative 6; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIPICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/723752
FILING DATE: 27-NOV-2000
APPLICATION NUMBER: 08/908469
FILING DATE: 06-AUG-1997
APPLICATION NUMBER: 08/833504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: Callfornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/10974591 Publication No. US20050112126A1 GENERAL INFORMATION:
            Application US/10861049
No. US20050095243A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Cui, Steven X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Baca, Manuel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-861-049-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-974-591-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     કે
```

```
1 DIQMIQSPSSLSASVGDRVIITCRASQSISNYLAWYQQKPGKAPKLLIYAASSLSSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIQMIQSPSSLSASVGDRVIITCRASQSISNYLAWYQQKPGKAPKLLIYAASSLESGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gian Gong
APPLICANT: Gian Gong
TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
FILE REFERENCE: P204 GOLF!
CURRENT APPLICATION NUMBER: US/11/021,874
FRIOR APPLICATION NUMBER: US 10/861,049
PRIOR APPLICATION NUMBER: US 60/476,531
PRIOR APPLICATION NUMBER: US 60/476,481
PRIOR APPLICATION NUMBER: US 60/476,481
PRIOR APPLICATION NUMBER: US 60/476,481
PRIOR PILING DATE: 2003-06-05
PRIOR FILING DATE: 2003-06-05
PRIOR FILING DATE: 2003-06-05
NUMBER OF SEQ ID NOS: 165
SEQ ID NOS: 165
                                                                                                                                                                                                                                                                                                                                                                                                                   61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSLPWTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSLPWTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                    61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNBYPLTFGQGTKVEIKR 108
                                                                                                                                                                  Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 506; DB 6; Length 108;
Pred. No. 1.2e-34;
6; Mismatches 5; Indels
                                                                                                                                                                                                                     5; Indels
                                                                                                                                                            Score 506; DB 5;
Pred. No. 1.2e-34;
6; Mismatches 5;
                                          TOPOLOGY: Linear SEQUENCE DESCRIPTION: SEQ ID NO: 12: US-10-974-591-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-11-021-874-38; Sequence 38, Application US/11021874; Publication No. US2005016377581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-811-123-6
, Sequence 6, Application US/09811123
; Patent No. US2002001587A1
, GENERAL INFORMATION:
LENGTH: 108 amino acids TYPE: Amino Acid
```

```
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIQMIQSPSSLSASVGDRVIITCRASQSISNYLAWYQQKPGKAPKLLIYAASSLESGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DIQMIQSPSSLSASVGDRVIIITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIQMIQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Сарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSLPWTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RPSGSGSGTDFTLTISSLQPEDFATYYCQQHNBYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 506; DB 4; Length 110;
Pred. No. 1.3e-34;
6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 109;
                TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-FEBE
TITLE OF INVENTION: ANTIBODY-MAYTANSINOID CONJUGATES
FILE REPRENCE: GENERIT. 073-25
CURRENT APPLICATION UNMBER: US/9/811,123
CURRENT PILING DATE: 2001-03-16
FRICH APPLICATION NUMBER: 05/238,327
FRICH APPLICATION NUMBER: 05/602,530
FRICH FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FASTESEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 90.4%; Score 506; DB 3; Length 10; Best Local Similarity 89.8%; Pred. No. 1.2e-34; Matches 97; Conservative 6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/10044896

Publication No. US20030166228A1

GENERAL INPORMATION:
APPLICANT: Chuntharapai, Anan
APPLICANT: Chuntharapai, Anan
APPLICANT: Cheste, Loonard G.
ITILE OF INVENTION: ANTI-INTERFERON-ALPHA ANTIBODIES
FILE REFERENCE: GENENT: 074A
CURRENT FILING DATE: 2002-01-09
PRIOR APPLICATION NUMBER: 60/270775
PRIOR APPLICATION NUMBER: 60/270775
PRIOR PILING DATE: 2001-02-22
NUMBER: OF SEQ ID NOS: 14
SCOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 110
                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Humanized Antibody Sequence US-09-811-123-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
US-09-809-739-10
'Sequence 10, Application US/09809739
'Petent No. US20020106369A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 90.4%;
Best Local Similarity 89.8%;
Matches 97; Conservative (
                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial Seguence
Mark Sliwkowski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-044-896-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JS-10-044-896-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               쉱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
```

Sednence Sed

```
DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 560; DB 2; Length 108; 100.0%; Pred. No. 7e-42; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
TITLE OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                      US-09-025-769B-43
US-09-490-070A-43
US-09-490-153-28
US-09-490-153-43
US-09-490-153-43
US-09-157-370-3
US-09-157-370-3
US-09-157-370-3
US-09-157-370-3
US-09-157-370-3
US-09-157-370-3
US-09-157-370-3
US-09-157-370-3
US-09-157-370-3
US-09-490-070A-14
US-09-490-153-14
US-09-490-153-14
US-09-490-153-14
US-09-490-153-14
US-09-490-153-14
US-09-490-153-14
US-09-90-153-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,899
                                                                                                                                                                                                                                              US-09-192-854-2
                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/225-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
                                                                                                                                                                                                                                                                                                                                                  US-08-974-899-2; Sequence 2, Application US/08974899; Patent No. 6037454; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILLING DATE: 11/27/96
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino Acid
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-974-899-2
Query Match
Best Local S
Matches 108
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 47, Appl
Sequence 3, Appli
Sequence 12, Appli
Sequence 10, Appli
Sequence 3, Appli
                                                                                                April 13, 2006, 17:19:00 ; Search time 31.5983 Seconds (without alignments) 282.578 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18, Sequence 18, Sequence 18, Sequence 14, Sequence 18, Sequence 18, Sequence 18, Sequence 5, A
                                                                                                                                                                                      1 DIQMTQSPSSLSASVGDRVT.....QQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
               GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                        Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PGTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-974-899-2

US-09-795-798-2

US-08-027-449-47

US-08-027-95-47

US-09-121-952A-47

US-09-1234-340A-47

US-09-355-014-47

US-09-355-014-47

US-08-975-798-3

US-08-979-10

US-08-795-798-3

US-08-795-798-3

US-08-795-798-3

US-09-705-398-3

US-09-705-398-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-648-067A-14
US-09-705-686-18
US-09-705-392A-18
US-09-705-398-18
US-09-602-812A-5
                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                            572060 seqs, 82675679 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                                  Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80
                                                                                                                                                         US-10-727-737-2
560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query
Match Length
                                                                                                                                                                                                                   BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
                                                                                                                                                                          Perfect score:
                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence:
                                                                                                                                                                                                                                                               Searched:
                                                                                                   Run on:
```

ö 9 9

Gaps

```
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIOMIOSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Gonzalez, Tania R.
APPLICANT: Beong, Steven R.
APPLICANT: Leong, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
                         RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNBYPLTFGQGTKVEIKR 108
61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 560; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 7e-42;
Matches 108; Conservative 0; Mismatches 0; Indels
                                                                                                                                     ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REGISTRATION NUMBER: 91014R1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-027-449-47; Sequence 47, Application US/09027449; Patent No. 6025158; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 108 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                  RESULT 2
US-09-795-798-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-795-798-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
                                    셤
  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
```

```
1 DIQMIQSPSSLSASVGDRVIITCRASKTISKYLAWYQQKPGKAPKLLIYYSGSTLESGVP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLI-YSGSTLQSGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4

US-08-804-444A-47

US-08-804-444A-47

Sequence 47, Application US/08804444A

Patent No. 6117980

GENERAL INFORMATION:
APPLICANT: Genzalz, Tania N
APPLICANT: Leong, Steven R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INFORMENCES:
TITLE OF INFORMENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE:
ADDRESSE:
CORRESPONDENCE Generatech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: CONTRY: USA
ZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 546.5; DB 2; Length
Pred. No. 1.1e-40;
1; Mismatches 0; Indels
                                                                                   ZUUNITER READABLE FORM:
MEDIUM TYPE: 35 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Withbatin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/027,449
FILING DATE: 20-Feb-1998
CLASSIFICATION A435
PRIOR APPLICATION A74:
APPLICATION NUMBER: 60/074,330
FILING DATE: 22-Jan-1998
PRIOR APPLICATION DATA: APPLICATION NUMBER: 60/038,664
FILING DATE: 21-Feb-1997
ATTORNEY/AGENT INFORMATION: NAME: LOVE, Richard B. REGISTRATION NUMBER: 34,659
REGISTRATION NUMBER: 36,052-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATE: APPLICATION NUMBER: US/08/804,444A
FILING DATE: 21-Peb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
                            South San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 98.2%;
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 109 amino acids
Amino Acid
DNA Way
                                               STATE: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-027-449-47
```

```
KESULT 6

US-09-121-952A-47

Squence 47, Application US/09121952A

Patent No. 6458355

GENERAL INFORMATION:
PAPPLICANT: Genenteh, Inc., Heei, Vanessa

APPLICANT: Leong, Steven R.

APPLICANT: Leong, Steven R.

APPLICANT: Shahrokh, Zahra

APPLICANT: Shahrokh, Inc.

APPLICANT: Shahrokh, In
1 DIOMIQSPSSLSASVGDRVIITCRASKTISKYLAWYQOKPGKAPKLLI-YSGSTLQSGVP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIONTOSPSSLSASVGDRVTITCRASKTISKYLAWYOOKPGKAPKLLIYYSGSTLESGVP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 SRFSGSGSGTDFTLTISSLOPEDFATYYCQOHNEYPLTFGGGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SRFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGGGTKVEIKR 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97.6%; Score 546.5; DB 2; Length 109; 98.2%; Pred. No. 1.1e-40; tive 1; Mismatches 0; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/121,952A
FILING DATE: 24-Jul-1998
CLASSIPICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/07430
FILING DATE: 22-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/075467
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, RICHARD B.
REGISTRATION NUMBER: 34,659
REGISTRATION NUMBER: 34,659
TELECOMMUNICATION:
TELEFHONE: 650/225-5530
TELEFHONE: 650/225-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 47: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 109 amino acida TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 97.6
Best Local Similarity 98.2
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIQMIQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYYSGSTLESGVP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLI-YSGSTLQSGVP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 47, Application US/09026985

Sequence 47, Application US/09026985

Patent No. 6131426

GENERAL INFORMATION:

APPLICANT: Leong, Steven R.

APPLICANT: Leong, Steven R.

TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS:

ADDRESSE: Genentech, Inc.

STREET: DNA Way

CITY: South Saw Francisco

STATE: California

CONTRICTOR CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 SRFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SRFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 97.6%; Score 546.5; DB 2; Length 109; Best Local Similarity 98.2%; Pred. No. 1.1e-40; Matches 107; Conservative 1; Mismatches 0; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.6%; Score 546.5; DB 2;
98.2%; Pred. No. 1.1e-40;
tive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATE:
APPLICATION DATE: 20-Feb-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, RICHARD B.
REGISTRATION NUMBER: 34,659
REGISTRATION NUMBER: 34,659
REGISTRATION NUMBER: 34,659
REGISTRATION NUMBER: 34,659
REGISTRATION NUMBER: 91095R3-1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                      ATTORNEY/AGENT INPORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085
TELEPONMUNICATION INPORMATION:
TELEPAX: 650/225-5530
TELEPAX: 650/225-9881
INPORMATION FOR SEQ ID NO: 47:
SEQUENCE TRARACTER.FILES:
LENGTH: 109 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 47:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 109 amino acids
Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 97.6
Best Local Similarity 98.2
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
LENGTH: 109 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: Linear
US-08-804-444A-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: Linear
   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-026-985-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ठ
```

```
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible COMPUTER: PC-DOS/MS-DOS SOFTWARE: PC-DOS/MS-DOS COFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Love, Richard B. REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3PCT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 47:
                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                               CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 109 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 650/225-5530
   Shahrokh, Zahra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                       NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 98.2 Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-355-014-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-974-899-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠ
Sequence 10. Seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DIGMTGSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYYSGSTLESGVP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DIOMIQSPSSLSASVGDRVIIICRASKIISKYLAWYQQKPGKAPKLLI-YSGSTLQSGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 SRPSGSGSGTDFTLTISSLQPEDFATYYCQQHNBYPLTFGQGTKVEIKR 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97.6%; Score 546.5; DB 2; Length 109; 98.2%; Pred. No. 1.1e-40; tive 1; Mismatches 0; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Genentech, Inc., Heei, Vanessa
Koumenis, Iphigenia
Leong, Steven R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: Withbatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,340A
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US/09/121,952
FILING DATE: 24-Jul-1998
APPLICATION NUMBER: 60/07430
FILING DATE: 22-JAN-1998
APPLICATION NUMBER: 60/07467
FILING DATE: 20-FEB-1998
ATTORNEY-AGENT INFORMATION:
NAME: LOVE, RICHARD B.
REGISTRATION NUMBER: 34,659
REFERENCE/POCKET NUMBER: 34,659
REFERENCE/POCKET NUMBER: 91085R4
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
TOWNTH: 109 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 47, Application US/09355014 Patent No. 6870033 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Presta, Leonard G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 109 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 98.2
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-234-340A-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-355-014-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
1 DIQMIQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYYSGSTLBSGVP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLI-YSGSTLQSGVP 59
Zapata, Gerardo A.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
Humanized Anti-IL-8 Monoclonal Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 SRFSGSGSGTDFTLTISSLQPEDFATYYCQQHNBYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 SRPSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97.6%; Score 546.5; DB 2; Length 109; 98.2%; Pred. No. 1.1e-40; tive 1; Mismatches 0; Indels 1
                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/355,014
FILING DATE: 21-Jul-1999
CLASSIFTCATION: cUnknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08974899
Patent No. 6037454
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSER: Genencech, Inc.
STREET: 1 DNA WAY
```

```
US-08-908-469-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                          셤
                                                                                                                                                                                                     è
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLAWYQQKPGKAPKLLIYAASSLESGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSLPWTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RPSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                     Score 506; DB 2; Length 108;
Pred. No. 3.6e-37;
6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Humanized Anti-CD11a Antibodies NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/9/795,798 FILING DATE: 28-Peb-2001
CLASSIFICATION: <u >Unknown></u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: <UNKNOWN:
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 11/27/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 91014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/22-1994
TELEPHONE: 650/22-1994
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/09795798
Patent No. 6703018
GENERAL INFORMATION.
APPLICANT: Presta, Leonard G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                                                                                         90.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 3
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 89.8 Matches 97; Conservative
                                                                                                                                                                                                                                                                                                        TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                JS-08-974-899-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -09-795-798-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-795-798-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                  1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS 60
                                                                                                                              1 DIQMIQSPSSLSASVGDRVIITCRASQSISNYLAWYQQKPGKAPKLLIYAASSLESGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLAMYQQKPGKAPKLLIYAASSLESGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIOMIGSPSSISASVGDRVIIICRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                     Gaps
                                                     ö
                                                                                                                                                                                                                              61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSLPWTFGQGTKVEIKR 108
                                                                                                                                                                                                61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 RPSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSLPWTFGQGTKVEIKR 108
90.4%; Score 506; DB 2; Length 108; 89.8%; Pred. No. 3.6e-37; live 6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 90.4%; Score 506; DB 2; Length 10. Best Local Similarity 89.8%; Pred. No. 3.6e-37; Matches 97; Conservative 6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DS/MS-DOS SOFTWARE: Winpatin (Genentech) CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/908,469
FILING DATE: 21-May-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: 08/933,504
FILING DATE: 07-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093P1
TELECOMMUNICATION INFORMATION:
TELEPAX: 650/25-9674
INFORMATION POR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: Linear SEQ ID NO: 12: US-08-908-469-12
                                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application US/08908469
Patent No. 6884879
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94080
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Baca, Manuel
Query Match
Best Local Similarity 89.8
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
```

```
REGISTRATION NUMBER:
                                                                                                                                                                                                                     US-07-934-373C-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-437-642B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 DIQMTQSPSSLSASVGDRVTITCKASKSISNYLAWYQQKPGKAPKLLIYYGSTLRSGVPS 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 505; DB 2; Length 127;
Pred. No. 5.2e-37;
4; Mismatches 6; Indels
                             Sequence 10, Application US/09809739
Patent No. 6663863
GERREAL INFORMATION:
APPLICANT: Horvath, Christopher J.
TITLE OF INVENTION: Method of Inhibiting Stenosis and TITLE OF INVENTION: Retenosis
FILE REFERENCE: 1855.1069-003
CURRENT APPLICATION NUMBER: US/09/809,739
CURRENT PILING DATE: 2001-03-15
PRIOR PILING DATE: 2001-03-17
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZUDANTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genericch) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C FILING DATE: 21-Aug-1992 CLASSIFICATION DATA: APPLICATION DATA: APPLICATION DATA: PRILING DATE: 15-JUN-1992 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/715272 FILING DATE: 14-JUN-1991 ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/07934373C
Sequence 1, Application US/07934373C
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Genericch, Inc. STREET: 1 DNA Way CITY: South San Francisco COUNTR: UsA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 90.7%;
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Lee, Wendy M
             -09-809-139-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-07-934-373C-3
                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઢ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
```

```
1 DIOMIOSPSSLSASVGDRVIIICRASKIISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIOMIQSPSSLSASVGDRVTITCRASQDVSSYLAWYQQKPGKAPKLLIYAASSLESGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-146-206C-3

| Sequence 3. Application US/08146206C
| Partent No. 6407213
| Partent No. 6407213
| APPLICANT: Carter, Paul J.
| APPLICANT: Presta, Leonard G.
| TITLE OF INVENTION: Method for Making Humanized Antibodies NUMBER OF SEQUENCES: 26
| CORRESPONDENCES: 26
| ADDRESSPEN: Generatech, Inc. STREET: 1 DNA Way
| CITY: South San Prancisco | STATE: California | STATE: California | COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSLPYTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RPSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RPSGSGSGTDPTLTISSLQPRDPATYYCQQHNBYPLTPGQGTKVEIKR 108
                                                                                                                 Query Match 90.0%; Score 504; DB 2; Length 109; Best Local Similarity 88.9%; Pred. No. 5.4e-37; Matches 96; Conservative 6; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 90.0%; Score 504; DB 2; Length 109; Best Local Similarity 88.9%; Pred. No. 5.4e-37; Matches 96; Conservative 6; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: DATE OF THE COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Windatin (Genentech) CURRENT APPLICATION NUMBER: US/08/146,206C FILING DATE: 17-No. 6407213-1993 CLASSIFICATION S30 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/715272 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/715272 PRIOR APPLICATION NUMBER: 07/715272 PRIOR APPLICATION NUMBER: 07/715272 PRIOR APPLICATION NUMBER: 90709P1 TELECOMMUNICATION INFORMATION: S0709P1 TELECOMMUNICATION INFORMATION: 550/252-9801 TELECOMMUNICATION S07052-9801 INFORMATION POR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LEMPACHER STRICE: L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: April 13, 2006, 17:20:47 Job time : 32.5983 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: Linear
US-08-146-206C-3
Linear
; TOPOLOGY:
US-08-437-642B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

### THIS PAGE IS BLANK

```
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
```

OM protein - prot Run on: A		OM protein - protein search, using sw model	April 13, 2006, 17:05:54 ; Search time 140.07 Seconds (without alignments) 543.993 Million cell updates/sec
OM protein - Run on:	dan	protein a	April
		OM protein -	Run on:

	DIOMTQSPSSLSASVGDRVTQQHNEYPLTFGQGTKVEIKR 108	
US-10-727-737-2	1 DIQMTQSPSSLSASVGDRVT	
Title: US-:	Sequence:	

2166443 seqs, 705528306 residues Scoring table: BLOSUM62 Gapop 10.0, Gapext 0.5 Searched:

2166443 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries UniProt\_05.80:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

			sapien	sapien		sapien	sapien	sapien	sapien			sapien	sapien	sapien		sapien	sapien	sapien	sapien				sapien	sapien	sapien	sapien	sapien	sapien	sapien	sapien	sapien	sapien	sapien
	tion		homod	homod	homod	homo	homod	homod	рошо	homo	рошо	homo	homod	homod	homo	homo	homo	homo	рошо	homo	рошо	homo	рошо	homo	рошо	homo	рошо	рошо	homo	homo	рошо	рошо	рошоч
	Description		Q6gmx8	P04430	Q7z3y4	09u170	Qegmx9	Q6pih7	Q6gmw1	Q9u177	P01600	Q968a9	Q502w4	Q65zc8	Q65zc9	P01605	Q7z473	Qegmx0	Q9u179	P01599	P01604	P01611	P01596	P01594	P04431	Q6pit5	P01598	P01607	P01610	P01606	P01608	P80362	Q9u181
	a		DEGMIXB HUMAN	KV1V HUMAN	Q7Z3Y4 HUMAN	Q9UL70 HUMAN	DEGMX9 HUMAN	Q6PIH7 HUMAN	QGGMW1 HUMAN	29UL77 HUMAN	KV1H HUMAN	296SA9 HUMAN	Q502W4 HUMAN	Q652C8 HUMAN	1652C9 HUMAN	KV1M HUMAN	27Z473 HUMAN	26GMX0_HUMAN	Q9UL79_HUMAN	CV1G_HUMAN	KV1L HUMAN	KV1S HUMAN	KV1D HUMAN	KV1B_HUMAN	KV1W_HUMAN	DEPITS HUMAN	KV1F HUMAN	KV10 HUMAN	KV1R HUMAN	KV1N HUMAN	CV1P HUMAN	KV1Y HUMAN	29UL81_HUMAN
		:	<u>.</u>	<b>*</b>	٠ م	~	٠ م	۵	~	~	æ. 	<u>د</u>	٠ م	~	~	×.	~	~	~	×,	æ. 	<b>*</b>	<b>*</b>	×.	×	<u>ن</u>	<b>*</b>	*	<b>2</b> 4	×.	×.	×	
	20	į		_		_				~	_	_		-		_	-		~	_	_	_	_	_	_		_	_	_	_	_	_	_
	Query Match Length DB		236	108	236	108	236	236	236	301	108	107	236	244	240	108	234	236	108	108	108	108	107	108	129	236	108	108	108	108	108	108	107
<b></b>	Match		86.8	85.9	85.9	85.5	85.5	85.4	85.0	4	84.6	84.6	84.1	84.1	83.9	82.9	82.7	82.7	82.5	82.3	82.3	82.1	81.9	ч	81.8	81.4	_	81.2	~	80.7	80.7	80.7	90.6
	Score		486	481	481	479	479	478	476	475	474	473.5	471	471	470	464	463	463	462	461	461	460	458.5	458	458	456	455	455	455	452	452	452	451.5
1	No.		1	7	m	4	ß	9	7	80	σ	10	11	12	13	. 14	,15	16	17	18;	19	20	21	22	23	24	25	26	27	28	29	30	31

108 1 KVIK HUMAN 1236 2 G6PIH4 HUMAN 108 1 KVIQ HUMAN 108 1 KVIQ HUMAN 1234 2 G5EREG HUMAN 108 2 G56917 HUMAN 108 1 KVIA HUMAN 117 1 KVII HUMAN 117 1 KVII HUMAN 117 1 KVII HUMAN 118 1 KVII HUMAN 119 1 KVII HUMAN 116 2 G96PFG HUMAN 119 1 KVII HUMAN 119 1 KVII HUMAN 110 1 KVII HUMAN	P01603 homo sapien O6pih4 homo sapien P01597 homo sapien P01609 homo sapien O5efe6 homo sapien P01593 homo sapien P01602 homo sapien P01601 homo sapien P01601 homo sapien P01501 homo sapien P01512 homo sapien P01512 homo sapien P01612 homo s
20000000000000000000000000000000000000	KV1K HUMAN Q6PIH4 HUMAN KV1Q HUMAN Q5EFEG HUMAN Q56917 HUMAN KV1X HUMAN KV1X HUMAN KV1J HUMAN KV1J HUMAN KV1J HUMAN KV1J HUMAN KV1T HUMAN
	20000000000000000000000000000000000000
800.24 400.28 700.88 700.89 700.70 700.70 700.80	450 449 447 442 442 443 443 431 428 428 428 428 423 423 412
	WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW

### ALIGNMENTS

N

88 B B

è

용

8 유

```
**X. Tabbas-Kartarian Mandaca: 2477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Atlausperg R.L., Feingold E.A., Grouse L.H., Derge J.G., Atlausperg R.L., Seingold E.A., Grouse L.H., Derge J.G., Mattenar R.D., Colling F.S., Wagner L., Schaefer C.F., Bhat N.K., Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haide F., Bartechenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Caavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Frange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunarane P.H., Nakharasha S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Wilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Schmutz J., Myers R.M., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones J.M., Marra M.A., Sche
      1 DIQLTQSPSSLSASVGDRVTITCRASQSVYNYVAWFQQKPGKAPKSLIYDASTLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                               61 RPSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                          61 NFTGSGSGTDFILTISSLQPEDFATYYCQQYNSYPYTFGQGTKVQIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          th 85.9%; Score 481; DB 2; Length 23 [Similarity 85.2%; Pred. No. 6.2e-41; 92; Conservative 7; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25702 MW; 7FBFE4ED23084BC6 CRC64;
                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nd mouse cDNA sequences.";
roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                            236 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWARTS, SNOWSTEE, ST. PROSITE; PROSITE; PS50835; IG LIKE; 2. PROSITE; PS00290; IG MHC; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, BC005332; AAH05332.1; -; mRNA.
HSSP; P01834; 1HEZ.
Rnsembl; RNSG00000163245; Homo sapiens.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003506; Ig_WHC.
InterPro; IPR003596; Ig_WHC.
IREPRO; IPR003596; Ig_WHC.
ISERM; PR07654; C1-864; I.
SMART; SM00406; IGY!
                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                              01-0CT-2003 (TrEMBLrel. 25, 01-0CT-2003 (TrEMBLrel. 25, 01-MAR-2004 (TrEMBLrel. 26, Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                   Q7Z3Y4_HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Skeletal Muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Skeletal Muscle,
                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                             0723Y4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                               셤
                                                                                                                                                                                            셤
                                          ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                       1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS 60
                                                                                                                                                                                                                                82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                 23 DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIOMIQSPSSLSASVGDRVTITCRASKIISKYLAWYQQKPGKAPKILIYSGSTLQSGVPS
                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #EDLINE=86174817; PubMed=3083240; DOI=10.1016/0161-5890(86)90173-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dwulet F.E., O'Connor T.P., Benson M.D.;
"Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
Mol. Immunol. 23:73-78(1986).
                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A01878; KIHUBN.
HSSP; P80362; 1WTL.
SMR; P04430; 1-108.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0003823; F:antigen binding; NAS.
HCO; GO:00003825; F:lammune response; NAS.
InterPro; IPR003109; Ig-1ike.
InterPro; IPR003596; Ig-v.
SNART; SM00406; IGv; 1.
PROSITE; PS50835; IG-LIKE; 1.
Amyloid; Direct procein sequencing; Immunoglobulin domain;
Immunoglobulin V region.
                                                                                                                                                                                                                                                                      61 RPSGSGSGTDFTLTISSLQPEDPATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                              Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complementarity-determining-1. Pramework-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complementarity-determining-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complementarity-determining-3
                                                                                                      Score 486; DB 2; Length 23
Pred. No. 1.9e-41;
8; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Indels
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS50029; IG MHC; UNKNOWN 1.
SEQUENCE 236 AA; Z5707 MW; 4FC8E14B6559EFC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11840 MW; CD3FD944FE96FD37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 481; DB 1;
Pred. No. 2.5e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-AUG-1987 (Rel. 05, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                      108 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Framework-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig kappa chain V-I region BAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-AUG-1987 (Rel. 05, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85.9%;
                                                                                                        86.84;
                                                                                                                           86.1%;
                                                                                                                                             93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90;
                                                                                                                                                                                                                                                                                                                                                                                                                   KV1V HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON TER
SEQUENCE
                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULPID
                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGION
REGION
REGION
REGION
                                                                                                                                                                                                                                                                                                                                                                                            P04430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loca
Matches
                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                             RESULT 2
```

```
23 DIQMTQSPSSLSASVGDTVTITCRASQDISNYLAWFQQKPGKAPKSLIYGASSLQSGVQS 82
DIOMTOSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
```

ö

0; Gaps

Length 236;

```
NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IGKC protein. .
Name=IGKC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT O
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKSLIYAASTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIOMTOSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLOSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Manheimer-Lory A., Katz J.B., Pillinger M., Ghossein C., Smith A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diamond B.;
"Molecular characteristics of antibodies bearing an anti-DNA-
associated idiotype.";
J. Exp. Med. 174:1639-1652 (1991).
EMBL; AF035044; AAD56280.1; -; mRNA.
PIR; PR0863; PR0863.
SMR; Q9UL70; 1-108.
KPSGSGSGTDFTLTISSLQPEDFATYYCQQYKSYPVTFGQGTKLEIKR 130
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RPSGSGSGTDPTLTISSLQPEDPATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85.5%; Score 479; DB 2; Length 108; 86.1%; Pred. No. 4e-41; tive 5; Mismatches 10; Indel8
                                                                                                                                                                     01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          '4e-41;
-hes 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clin. Immunol. Immunopathol. 87:184-192(1998).
                                                                                                        108 AA
                                                                                                          PRT;
                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR007110; Ig-like.
InterPro; IPR00359; Ig-v.
SWART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-2004 (TIEMBLrel. 27, 05-JUL-2004 (TIEMBLrel. 27, 05-JUL-2004 (TIEMBLrel. 27,
                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                        QQUL70 HUMAN PRELIMINARY;
QQUL70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QGGMX9 HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=1660528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GKC protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fetus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MANDE
                                                             RESULT 4

QUILLO DO HU

DE 01-M

DE 01-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

```
TISSUB-Primary B-Cells,

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Ratusherg R.L., Tesingold B.A., Grouse L.H., Derge J.G.,

A Lischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A phykins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A branchen M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Perers G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahey J., Helton B., Ketteman M., Madan A., Rouffard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodiguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield X.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield X.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Roberzation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 DIQMTQSPSSLSASVGHRVTITCRASQNVSRMLAWYQQRPEKAPKSLIYATSSLHSGVPS 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapions (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNTYPLTFGGGTKVEIKR 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.5%; Score 479; DB 2; Length 23
85.2%; Pred. No. 9.9e-41;
ive 8; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (JUN-2004) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG WHC; UNKNOWN 1.
SEQUENCE 236 AA; Z5924 MW; FDE2093DC560CFF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMR; Q6GMX9; 23-236.
Ensembl; ENSG0000163245; Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; BC073763; AAH73763.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003066; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF07654; Cl-8et; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QEPIH7 HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART, SM00409, IG, 2.
SMART, SM00407, IGc1, 1.
SMART, SM00406, IGv, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Primary B-Cells;
NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE
```

ô

```
Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Nauberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Nauberg R.L., Straubberg R.L., Colling F.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., Brangleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Frange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Britards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Wilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glbbs R.A., Pathon B., Ketreman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 IQMTQSPSSLSASVGDRVTITCRASQGISNDLGWYQQKPGKAPKLLIYAASSLQSGVPSR 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 IQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPSR
                                       MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 FSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSGSGSGTDFTLTISSLQPEDFATYYCLQDYNYPWTFGGGTKVEIKR 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q<u>UL77</u> HUMAN PRELIMINARY; PRT; 108 AA.
Q9UL77.
Q9UL77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IRR003599; Ig.
InterPro; IRR003110; Ig-like.
InterPro; IRR0031006; Ig-like.
InterPro; IRR003006; Ig-MrC.
InterPro; IRR003596; Ig-V.
Pfam; PRO7654; CL-set; I.
SWART; SW004007; IG-2.
SWART; SW004007; IG-1; I.
SWART; SW00407; IG-1; I.
PROSITE; PSS0835; IG LIKE; 2.
PROSITE; PSS0835; IG LIKE; 2.
PROSITE; PS08399; IG MrG; UNKNOWN 1.
SEQUENCE 236 AA; Z5751 MW; SBFE6A087APAC437 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH MGC Project;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databages.
EMBL; BC073791; AAH73791.1; -; mRNA.
SWR; QGGMM1; 24-236.
ENBembl; ENSG0000163245; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.0%; Score 476; DB 2
87.9%; Pred. No. 2e-40;
tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 87.9 es 94, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rissum=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                           RA Strausberg R.L., Feligold B.A., Grouse L.H., 1073/pnas.245603899;

R. Klausner R.D., Colline F.S., Wagner L., Shemmen C.M., Schuler G.D.,

R. Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

R. Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

R. Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Haleh F.,

R. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hang L.,

R. Stapleton M., Soares M.B., Bonaldo M.F., Casawant T.L., Scheetz T.E.,

R. Brownstein M.J., Udgidn T.B., Toshlywik S., Carninch F., Frange C.,

R. Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

R. Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,

W. Villalon D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A.,

R. Hitching M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Beneration and initial analysis of more than 15,000 full-length human

R. Tand mouse CDNA sequences.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 DIQLTQSPSFLSASVGDRVTITCRASQGISSYLAWYQQKPGKAPNLLIYAASTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIOMTOSPSSLSASVGDRVTITCRASKTISKYLAWYQOKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                   (EDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RESCISSIOPTLIISSLQPEDFATYYCQQHNEYPLIFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RFSGSGSGTEFTLTISSLOPEDFATYYCOOLNSSPPTFGGGTKVEIKR 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH MGC Project;

NIH MGC Project;

Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

R MSSP; POLG67; 1A2.

R MSSP; POLG7; 123-236.

R Ensembl; RNG3000015345; Homo sapiens.

R InterPro; IPR007110; Ig-1ike.

R InterPro; IPR007599; Ig.

R InterPro; IPR003599; Ig.

R InterPro; IPR003596; Ig.

R InterPro; IPR003596; Ig.

R SWART; SM00409; IG.;

R SWART; SM00409; IG.;

R SWART; SM00406; IG.;

R SWART; SWART; SM00406; IG.;

R SWART; SWART; SW00406; IG.;

R SWART; SW00406; IG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.4%; Score 478; DB 2; Length 236; 87.0%; Pred. No. 1.3e-40; tive 4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
SEQUENCE 236 AA; Ž5603 MM; 8BG561106861213F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QGGMW1 HUMAN PRELIMINARY;
QGGMW1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKC protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Simi
Matches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rissum=Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HUMAN
```

SORR BERNERS REPORTED TO THE REPORT OF THE T

ö

Gape

ö

10; Indels

MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;

NUCLEOTIDE SEQUENCE NCBI\_TaxID=9606;

[1] NUCLEOTIDE SEQUENCE.

NCBI\_TaxID=9606;

RESULT 7

셤 ሯ 셤

```
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=1516616; Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.; Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.; "Human monoclonal striational autoantibodies isolated from thymic lymphocytes of patients with myasthenia gravis use VH and VL gene segments associated with the autoimmune repertoire."; Eur. J. Immunol. 22:2231-2236(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIJUE=98375893; PubMed=9712075; Adderson B.E., Shikhman A.R., Ward K.E., Cunningham M.W.; Molecular analysis of polyreactive monoclonal antibodies from rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQNYITPTSFGQGTRVEIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               By similarity.
                                                                                                                                                                                                                                                                                                                                              Framework-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                Framework-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pramework-4.
                                                                                                                                                                                                                                                                                                                                                                                      Framework-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibody V region genes.";
J. Immunol. 161:2020-2031(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        variable region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q96SA9 HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                            23
34
49
88
107
107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
PubMed=8436174;
                                                                                                        PIR; A01868; K1HUHU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGION
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN
                                                                  removed
                                                                                                                                                                                                                                                                                                                                                                                 REGION
REGION
REGION
REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q96SA9;
                                                                                                                                                                                                                                                                                                                                            REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This Swiss-Prot entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata, Craniata, Vertebrata, Buteleostomi;
Evarchontoglires, Primates; Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPNLLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                                                                                                                                                                                                       Wagner S.D., Luzzatto L.; "V kappa gene segments rearranged in chronic lymphocytic leukemia are distributed over a large portion of the V kappa locus and do not show
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                              Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.; "Human monoclonal striational autoantibodies isolated from thymic B lymphocytes of patients with myaethenia gravis use VH and VL gene segments associated with the autoimmune repertoire."; Bur. J. Immunol. 22:2231-2236(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Watanabe S., Hilschmann N.;
"The primary structure of a monoclonal kappa-type immunoglobulin I
chain of subgroup I (Bence-Jones Protein Hau): subdivision within
                                        Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
-1- MISCELLANEOUS: The C region of this chain has the INV (3)
-1- MISCELLANEOUS: This is a Bence-Jones protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESISTENTIALITIESTOPEDPATYYCQOSYSTSWTFGEGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFSGSGSGTDPTLTISSLQPEDPATYYCQQHNEYPLTFGQGTKVEIKR 108
Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 475; DB 2; Length 108;
Pred. No. 1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108 AA; 11738 MW; C06681716C4D16F3 CRC64;
                                                                                  21in. Immunol. Immunopathol. 87:184-192(1998)

    Last sequence update)
    Last annotation update)

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ensembl; ENSG0000163245; Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                            Eur. J. Immunol. 23:391-397(1993).
EMBL; AF035037; AAD56273.1; -; mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=71032830; PubMed=4097974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig kappa chain V-I region Hau. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR007110; Ig-like
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; B49047; B49047.
PIR; S34083; S34083.
HSSP; P01607; 1BWW.
SMR; Q9UL77; 1-108.
                                                                                                                          NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                          somatic mutation."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN SEQUENCE
                                                                                                                                                                                                                                                                                                                     PubMed=8436174;
                                                                                                                                              PubMed=1516616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LO-MAY-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       subgroups."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KV1H HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                    found D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P01600;
                                                                Ēetuв.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KV1H HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
REPLANTANT REPLANTANT REPLANTANT REPLANTANT REPLANTANT REPLANT REPLANTANT REPREPART REPREP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
```

m

```
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIQMIQSPSSLSASVGDRVTITCRASQSISSYLSWYQQKPGKAPQVLIYAASSLPSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DIOMIOSPSSISASVGDRVIIICRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                     PDB; 1F6L; X-ray; L=1-108.
GO; GO:0005576; C:extraccllular region; NAS.
GO; GO:0005576; C:extraccllular region; NAS.
GO; GO:0005953; P:antigen binding; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
PROSITE; PS50835; IG_LIKE; I.
PROSITE; PS50835; IG_LIKE; I.
D-structure; Bence-Jones protein; Direct protein sequencing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complementarity-determining-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complementarity-determining-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complementarity-determining-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RFSGSGSGTDFTLTISSLOPEDFATYYCOOHNEYPLTFGOGTKVBIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84.6%; Score 474; DB 1; Length 10
84.3%; Pred. No. 1.3e-40;
.ive 10; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11671 MW; 08D3A6160D8D0618 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunoglobulin domain; Immunoglobulin V region.
```

RATTA KARAKA KA

```
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McBwan P.J., McKernan K.J., Malek J.A., Gunaretne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Shevchenko Y., Boutfard G.G., Buterfield Y.S.N., Krzywinski M.I., Skalaka U., Smallus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marxa M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIFAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RPSGSGSGTDPTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MCLEOTIDE SEQUENCE.
MEDLINE-97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;
MCOATE-mann R.E., Wing M.G., Winter G.;
"Contement recruitment using bispecific diabodies.";
Nat. Biotechnol. 15:629-631(1997).
EMBL; Y13057; CAA73500.1; -; mRNA.
InterPro; IRR007599; Ig.
InterPro; IRR007110; Ig-like.
InterPro; IRR003599; Ig_w.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IRRO03059; IG.
InterPro; IRR007110; Ig-like.
InterPro; IRR007110; Ig-like.
InterPro; IRR003006; Ig-MHC.
InterPro; IRR003006; Ig-MHC.
InterPro; IRR003006; Ig-MHC.
InterPro; IRR00306; Ig-MHC.
InterPro; IRR00409; IG; IG-SMART; SM00409; IG; IG-SMART; SM00400; IG; IG-SMART; SM00400; IG-SMART; IG-SMART; SM00400; IG-SMART; IG-SMART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BC095489; AAH95489.1; -; mRNA.
SMR; Q502W4; 23-236.
Ensembl; ENSG0000163245; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GESCG HUMAN PRELIMINARY; PRT; 244 AA.
GESCG;
55-0CT-2004 (TrEMBLrel. 28, Created)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84.1%; Score 471; DB 2;
84.3%; Pred. No. 6.6e-40;
iive 7; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Glandular pool- thyroid;
NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Single-chain Fv (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=scFv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIQMIQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DIOMTOSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                 "V kappa gene segments rearranged in chronic lymphocytic leukemia are distributed over a large portion of the V kappa locus and do not show
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Glandular pool- thyroid;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
                                                                                                                                                                                                                                            Manheimer-Lory A., Katz J.B., Pillinger M., Ghossein C., Smith A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blaison G., Kuntz J.L., Pasquali J.L.; "Molecular analysis of V kappa III variable regions of polyclonal rheumatoid factors during rheumatoid arthritis."; Eur. J. Immunol. 21:1221-1227(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.6%; Score 473.5; DB 2; Length 107; illarity 88.0%; Pred. No. 1.5e-40; Conservative 5; Mismatches 7; Indels 1;
                                                                                                                                                                                                                                                                                                "Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMEL, U96396; AAB68765.1; -; mRNA.
PIR; B49047; B49047.
PIR; S16840; S16840.
PIR; S31977; S31977.
PIR; S34083; S34083.
PIR; S34085; S34086.
HSSP; POLGO7; IBWW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                      Eur. J. Immunol. 23:391-397(1993).
                                                                                                                                                                                                                                                                                                                                                         Exp. Med. 174:1639-1652(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SW00406; IGv; 1.
PR003TE; PS50815; IG LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OS02W4 HUMAN PRELIMINARY;
QS02W4;
         Wagner S.D., Luzzatto L.;
                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE
                                                                                              Bomatic mutation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                           PubMed=1660528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=1903706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IGKC protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Sim-
                                                                                                                                                                                                                                                                 Diamond B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=IGKC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
OS02W4_HUN
```

g ሯ 셤

ઠ

ö

Gaps ö

DB 2; Length 236;

10; Indels

9 82

```
PROTEIN SEQUENCE.
                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGION
DISULFID
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGION
  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                       1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                   61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                      197 RFSGSGSGTDFTLTISSLQPDDFATYYCQQYSNYPLTFGGGTKLRIKR 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RPSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RFSGSGSGTDFTLTISSLQPDDFATYYCQQYSNYPLTFGGGTKLEIKR 240
                                                                                                                                        Length 244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83.9%; Score 470; DB 2; Length 240;
82.4%; Pred. No. 8.5e-40;
ive 10; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97362799; Pubmed=9219263; DOI=10.1038/nbt0797-629;
                                                                                                                                                                             10, Indels
                                                                              244 244 247 AW; 4B1F17868338F2BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 AA; 25569 MW; FDCFD3645F64B373 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kontermann R.E., Wing M.G., Winter G.;
"Complement recruitment using bispecific diabodies.";
Nat. Biotechnol. 15:629-631(1997).
EMBL: Y19365, CAA73499.1; -; mRNA.
InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003599; Ig.
SMART; SM00409; IG; 2.
SMART; SM00406; IGv; 2.
PROSITE; PSS0835; IG_LIKE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                      84.1%; Score 471; DB 2;
82.4%; Pred. No. 6.8e-40;
tive 9; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 48, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KVIM HUMAN STANDARD; PR P01605; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last seque: 13-SEP-2005 (Rel. 48, Last annot: Ig kappa chain V-I region Lay.
SMART; SM00409; IG; 2.
SMART; SM00406; IGv; 2.
PROSITE; PS50835; IG_LIKE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single-chain Fv (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Q652C9 HUMAN PRELIMINARY;
Q652C9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 82.44
                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                        Query Match
Best Local Simi
Matches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=scFv;
                                                       NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KVIM HUMAN
ID KVIM HI
AC PO1605,
DT 21-JUL-
DT 13-SEP-
DB 19 kapi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                              SO THE PRESENCE OF THE PROPERTY OF THE PROPERT
    a
                                                                                                                                                                                                                                                                                                     ક
                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ठ
```

```
This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ERRATUM.

Goni F.R., Chen P.P., McGinnis D., Arjonilla M.L., Fernandez J.,
Carson D., Solomon A., Mendez E., Frangione B.;
J. Immunol. 143:3864-3864 (1989).

-!- MISCELLANEOUS: The second and third hypervariable regions of this chain are identical with those of the human POM V-III kappa chain, with which it shares certain idiotypic determinants.

-!- MISCELLANEOUS: This chain was isolated from an IGM with anti-gamma globulin activity.
                                                                                                                                                                                                                      Capra J.D., Klapper D.G.; "Complete amino acid sequence of the variable domains of two human IgM anti-gamma globulins (Lay/Pom) with shared idiotypic specificities."; Scand. J. Immunol. 5:677-684(1976).
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIQMIQSPSSLSVSVGDRVTITCQASQNVNAYLNWYQQKPGLAPKLLIYGASTREAGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=89215279; PubMed=2496160;
Goni F.R., Chen P.P., McGinnis D., Arjonilla M.L., Fernandez J.,
Carson D., Solomon A., Mendez B., Frangione B.;
Structural and idiotypic characterization of the L chains of human
IgM autoantibodies with different specificities.";
J. Immunol. 142:3158-3163(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RPSGSGSGTDFTFTISSLQPEDIATYYCQQYNNWPPTFGQGTKVEVKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RFSGSGSGTDFTL/ISSLQPEDFATYYCQQHNEYPL/FGQGTKVBIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complementarity-determining-1. 
Framework-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complementarity-determining-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Framework-3.
Complementarity-determining-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 464; DB 1; Length 10 Pred. No. 1.4e-39; 9; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11834 MW; 739993A95431434A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWART; SM00406; IGV; 1._
PROSITS; PS50835; IG_LIKB; 1.
Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; PO1607; 1BWW.

SWR; PO1605; 1-108

GO; GO:0005576; C:extracellular region; NAS.

GO; GO:0003823; F:antigen binding; NAS.

GO; GO:0006955; P:immune response; NAS.

InterPro; IPR007110; Ig-11ke.

InterPro; IPR00356; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Framework-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Framework-
                                                                                                                                                                                                  MEDLINE=77038198; PubMed=824717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82.9%;
                                                                                                                                                                                                                                                                                                                                                                 PROTEIN SEQUENCE OF 1-104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 80.6
1es 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23
34
49
88
107
108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A01871; K1HULY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24
35
50
57
89
98
108
108
```

```
TISSUB-LUNG,

WEDLINE-22380257, PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A phokins R.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,

Diatchenko L., Marusina K.R., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Boownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahesley N., Wuzny D.W., Sodergren B.D., Dickson M.C.,

Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rahesley R.W., Tochman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A.,

Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A.,

Radeneration and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81
                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSGSGSGTDFTLTISSLQPEDFATYYCQQHNRYPLTFGGGTKVBIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11arity 83.2%; Score 463; DB 2; Length 234; Sconstry 83.2%; Pred. No. 4.3e-39; Conservative 7; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brach 1, 24.2.2.

Brach 1, 200001631, 100001631, 100001631, 1000001631, 1000001631, 1000001631, 1000001631, 1000001631, 10000110, 10000110, 10000110, 10000110, 10000110, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000011, 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Lung;
NIH MGC Project;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC056556; AM566256.1; -; mRNA.
HSSP; P01834; 1HEZ.
SWR; Q72473; 222-234.
                                                                                                                                                                                  01-077-2003 (TrEMBLrel. 25, Created)
01-077-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                               234 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: April 13, 2006, 17:18:41
Job time : 141.07 secs
                                                                                                               PRT;
RESULT 15

O72473 HUMAN

ID Q72473 HUMAN PRELIMINARY;

AC 072473 (TERMELTEL 25,

DT 01-OCT-2003 (TERMELTEL 25,

DT 01-OCT-2003 (TERMELTEL 25,

DT 01-MAR-2004 (TERMELTEL 26,

DT MAR-2004 (TERMELTEL 26,

DT MAR-2004 (TERMELTEL 26,

C ENKARYOCE; Metazoa; Chordate

OC ENKARYOCE; Metazoa; Chordate

OC MOMEN SERVINE SEQUENCE.

RN 111

RN 111

RN 111

RA STRUBBERTS R.L., Felngold B.R.

RA STRUBBERTS R.D., Colling F.S.,

RA ALECHAR R.F., Zedebrg B.,

RA ALGENUS R.F., Zedebrg B.,

RA ALGARIES S., LOQUELLAND,

RA BENGAR S.R., MCEWAN P.J., MCI

RA BORLINE-22388257; PubMed=12,

RA ALGARIES R.R., MCEWAN P.J., MCI

RA ALGARIES R.R., MCEWAN P.J., MCI

RA RAHA S.S., LOQUELLAND N.A.,

RA RAHA S.S., LOQUELLAND N.A.,

RA RAHA S.S., LOQUELLAND D.N.,

RA RACHARGE S., WORLEY K.C., HR

RA WILLIAGN M., MCADA D.N.,

RA RACHARGE S., WORLEY K.C.,

RA ROLLING-2203, TOCHEMAN J.I.

RA MOLLEOTIDE SEQUENCE.

RY "Generation and initial and mouse cDNA sequences.";

RY "Generation and initial and mouse cDNA sequences.";

RY "Generation and initial and MULLEOTIDE SEQUENCE.

RY "Generation and initial and SRR; Q72473; 2-234,

DR RREEMD!, ENSGODO0163245; H

DR RREEMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
es 89; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
```

```
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
```

OM protein - protein search, using sw model

Run on:

April 13, 2006, 17:14:06 ; Search time 23.1092 Seconds (without alignments) 449.666 Million cell updates/sec

US-10-727-737-2 560 Title: Ferfect score:

1 DIQMTQSPSSLSASVGDRVT.....QQHNEYPLTFGQGTKVEIKR 108 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 segs, 96216763 residues

Searched:

Total number of hits satisfying chosen parameters:

DB seq length: 0 DB seq length: 200000000 Maximum I Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:\* 1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

### STIMMARTES

		•			SUMMAKIES	
Result No.	Score	Query Match	Length	DB	ID	Description
-	493	88.0	125	2	840333	Ig kappa chain V-J
7	490	87.5		~	B49047	
m	490	87.5	129	~	S40369	g kappa chain
4	489	87.3		~	846371	g kappa chain V-
2	487	87.0		~	S40349	kappa
9	487	87.0		~	840367	g kappa
7	486	86.8		~	S19674	kappa
ω	486	86.8		~	840331	kappa
0	486	86.8		7	S40352	kappa
10	484.5	86.5		7	840336	kappa c
11	483	86.2		~	S36264	g lambda
12	483	86.2		~	S40334	g kappa
13	481	85.9	108	Н	KIHUBN	g kappa
14	479	85.5		~	846372	light c
15	478	85.4		N	169017	ei-HIV1
16	476.5	85.1		~	836275	g lambda
17	476	85.0		7	846376	kappa
18	474	84.6		Н	KTHUHU	u
19	474	84.6		7	S36277	lambda
20	474	84.6		~	S38646	kappa
21	473	84.5		N	S26345	1 ight
22	473	84.5		~	831998	kappa chain
23	473	84.5		~	840353	kappa
24	473	84.5	127	N	S04574	kappa
25	472	84.3		~	844122	g kappa
56	471	84.1		~	840318	g kappa
27	469	83.8	125	~	S40316	kappa
28	467.5	•	108	~	S30521	g kappa c
59	466	ë.	108	~	S36279	

Ig kappa chain - h Ig kappa chain - h	kappa lambda kappa	19 kappa chain V r 19 kappa chain - h 19 kappa chain - h	kappa chain kappa chain	kappa chain kappa chain kappa chain	
S47182 S31981	S52793 S36269 K1HULY	S34007 S47183 S40370	S40350 S11240	K1HUGL K1HUKU S52789	K1HUWS I39154 S46370
0 0	224	000	00	Z	777
108	129 107 108	108	125	108 108 129	108 108 120
83.2	83.0 82.9 82.9	82.8 82.6 82.5	82.5	82.3 82.3 82.3	82.1 82.1 82.1
466 465	465 464 464	463.5 462.5 462	462 462	461 461 461	460 460 460
30	3 3 3 4 3 2	35 37	88	4 4 4 0 1 2	4 4 4 6 4 7

### ALIGNMENTS

```
A;Residues: 1-125 «KLE»
A;Residues: 1-125 «KLE»
A;Residues: UNIPARC:UPI0000116153; EMBL:X72443; NID:9441354; PIDN:CAAS1111.1; PII
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;34-108/Domain: immunoglobulin homology <IPM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: $40333
C;Accession: A60333
A;Klein, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: $40312; MUID:94080891; PMID:8258341
A;Accession: $40333
A;Atatus: preliminary; translation not shown
A,Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYKASSLESGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RESGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 88.0%; Score 493; DB 2; Length 125; I Similarity 86.9%; Pred. No. 3.2e-34; 93; Conservative 9; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

### B49047

Ig kappa chain V region (monoclonal striational autoantibody StrAB SA-1A) - human (fragme C;Species: Homo sapiens (man)
C;Accession: B49047
R;Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
Bur. J. Immunol. 22, 2231-2236, 1992
A;Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes (A;Reference number: A49047; MulD:92387224; PMID:1516616

A;Status: preliminary

A; Molecule type: nucleic acid
A; Molecule type: nucleic acid
A; Molecule type: nucleic acid
A; Residues: 1-108 < VIC>
A; Cross-references: UNIPROT: Q96SA9; UNIPROT: Q9UL77; UNIPARC: UPI0000176B44
A; Experimental source: thymic B lymphocytes
A; Note: sequence extracted from NCB1 backbone (NCBIN:113208, NCBIP:113209)
C; Superfamily: immunoglobulin V region; immunoglobulin homology < IMMA>

N

```
A;Cross-references: UNIPARC:UP10000116163; EMBL:X72459; NID:9441386; PIDN:CAA51127.1; PII CS.Superfamily: immunoglobulin v region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin v region; immunoglobulin homology F333-107/pomain: immunoglobulin homology < NMA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 IQLTQSPSSLSASVGDRVTITCRASQGISSALAWYQQXPGKAPKLLIYDASSLESGVPSR 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 DIQMTQSPSSLSASVGDVTITCRASQSISNYLNWYQRKPGKAPKLLIXAASSLQSGVPS 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DIQMIQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS 60
                                                                                                                                                                    CiSpecies: Homo sapiens (man)
CiDate: 19-May-1994 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
CiAccession: 540349
RiKlein, R.; Jaenichen, R.; Zachau, H.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig kappa chain V region (clone alpha-TEL9) - human
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C;Accession: S19674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.Species: Homo sapiens (man)
C.Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 IOMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPSR
                                                                                                                                                                                                                                                                            Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CjAccession: S40367
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40367
A;Status: preliminary; translation not shown
     68 RFSGSGSGTEFTLTISSLQPDDFATYYCQQYNSYFPPYTFGQGTKLEIKR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RPSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 FSGSGSGTDFTLTISSLQPEDFATYYCQQFNTYPLTFGGGTKVEIKR 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 FSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 487; DB 2; Length 127;
Pred. No. 1e-33;
5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPARC:UP10000176CB4; EMBL:X72477
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 487; DB 2;
Pred. No. 1e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.8%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                     A; Accession: S40349
A; Status: preliminary; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig kappa chain V-J-C region - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88.0%;
                                                                                                                                             Ig kappa chain V-J region - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 88.8 Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Residues: 1-125 < KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-127 < KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPARC:UPI0000116177; EMBL:X72479; NID:g441426; PIDN:CAA51147.1; PI C.Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPARC:UP100001165A4; EMBL:Z27172; NID:g415959; PIDN:CAA81696.1; PI CS.Superfamally: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin P;23-97/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RiBenaimon, C.; Chastagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A;Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene
A;Reference number: $46369; MUID:94313975; PMID:8039491
                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                9
                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 DIQMTQSPSSLSASVGDRVTITCRASHVISNHLVWFQQKPGKAPKSLIYAASSLQSGVPS 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63
                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig kappa chain V-J region (T24-3) - human (fragment)
C;Species: Homo applene (man)
C;Date: 27-Jan.1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C;Accession: S46371; S38645
                                                                                                                                             1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIQMIQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: $40369
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
R;Lein, R.; Jaenichen, R.; Zachau, H.G.
A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: $40312; MUID:94080991; PMID:8258341
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Gaps
                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RFSGSGSGTDFTLTISSLOPEDFATYYCOOHNEY--PLTFGOGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                     61 RFSGSGSGTDFTLTISSLOPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNBYPLTFGQGTKVEIKR 108
Score 490; DB 2; Length 108;
Pred. No. 5e-34;
4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 87.3%; Score 489; DB 2; Length 11 Best Local Similarity 85.5%; Pred. No. 6.5e-34; Matches 94; Conservative 9; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87.5%; Score 490; DB 2;
86.1%; Pred. No. 5.9e-34;
iive 7; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translation not shown
87.5%;
                                                   96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93; Conservative
                         Best Local Similarity
Matches 96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-129 < KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-117 <BEN>
                                                                                                                                                                                                                                                                                                                                                                                                                 Ig kappa chain - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: S4637]
  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loc
Matches
                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
```

ö

Gaps

ö

Gaps

m

ö

9 80

9 Š 셤

```
A;Cross-references: UNIPARC:UP1000116156; EMBL:X72446; NID:9441360; PIDN:CAA51114.1; PII C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;31-105/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S36264

Ig lambda chain V region (clone alpha-CEA4-8A) - human (fragment)

Ig lambda chain V region (clone alpha-CEA4-8A) - human (fragment)

Ig lambda chain V region (clone alpha-CEA4-8A) - human (fragment)

C; Species: Home sapiens (man)

C; Species: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000

C; Accession: S36564

R; Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.; BYBO J. 12, 725-734, 1993

A; Fitle: Human anti-self antibodies with high specificity from phage display libraries.

A; Reference number: S36256; MUID:93178448; PMID:7679990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-107 cGRI>
A;Residues: 1-107 cGRI>
A;Residues: 1-107 cGRI>
C;Reperfemily: immunoglobulin V region; immunoglobulin homology
C;Repwords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: $40318
C;Accession: $40318
Bur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: $40312; MUID:94080891; PMID:8258341
A;Accession: $40336
A;Accession: Sq0336
                                                                                                                                                                                                                                                                    21 DIOMIOSPSSLSASVGNRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLOSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 DIQLTQSPSFLSASVGDRVTITCRASQGISSYLAWYQQKPGKAPKLLIYAASTLQSGVPS
                                                                                                                                                                                                                                      1 DIOMIQSPSSLSASVGDRVIITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGXAPKLLIYSGSTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DIQMIQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEY-PLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 RFSGSGSGTEFSLTISSLQPEDFATYYCQQLATYPPWTFGQGTKVBIKR 124
                                                                                                                                                                                                                                                                                                                                                                                                     81 RFSGSGSGTDFSLTISSLQPEDVATYYCQKYNSVPRTFGQGTKVEIKR 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 124;
                                                                                                     Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 107;
                                                                                                                                                                                                                                                                                                                                                                61 RPSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR
                                                                                                     Score 486; DB 2; Length 13
Pred. No. 1.3e-33;
6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.2%; Score 483; DB 2; Length 10
86.0%; Pred. No. 1.9e-33;
ive 9; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86.5%; Score 484.5; DB 2; llarity 88.1%; Pred. No. 1.6e-33; Conservative 5; Mismatches 7;
      C;Keywords: heterotetramer; immunoglobulin P;36-110/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig kappa chain V-J region - human
                                                                                                  sch 86.8%; 1 Similarity 87.0%; 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 86.2
Best Local Similarity 86.0
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-124 < KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: S36264
                                                                                                     Query Match
Best Local S
                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                   ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠ
                                                                                                                                                                                      Agresidues: 1-108 - MAR>
Agresidues: 1-108 - MAR>
Agross-references: UNIPARC:UPI0000115FE1; EMBL:X61642; NID:g37860; PIDN:CAA43823.1; PID
Agross-references: UNIPARC:UPI0000115FE1; EMBL:X61642; NID:g37860; PIDN:CAA43823.1; PID
C,Superfamily: immunoglobulin to region; immunoglobulin homology
C,Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     П
R:Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. 292, 581-597, 1991
J. Mol. 292, 581-597, 1991
A:Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph. A:Reference number: $19663; MUID:92085276; PMID:1748994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cross-references: UNIPARC:UPI0000116151; EMBL:X72441; NID:9441350; PIDN:CAA51109.1; Superfamily: immunoglobulin V region; immunoglobulin homology Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Molecule type: mRNÅ
A,Residues: 1-131 «KIE»
A,Cross-references: UNIPARC:UPI0000116166; EMBL:X72462; NID:9441392; PIDN:CAA51130.1;
C,Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C_Species: Homo sapiens (man)
C_Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C_Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C_DAtcession: S4031
R_FKlein, R., Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 2348-3271, 1993
R_FILLE: Expressed human immunoglobulin chi genes and their hypermutation.
R_FREFERENCE number: S40312; MUID:94080891; PMID:8258341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CiSpecies: Homo sapiens (man)
Cibate: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
CiAccession: $40352
Rixlein, R.; Jaentchen, R.; Zachau, H.G.
Rixlein, R.; Jaentchen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: $40312; MUID:94080891; PMID:8258341
A;Accession: $40352
A;Status: preliminary; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RPSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RPSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 86.8%; Score 486; DB 2; Length 108; Local Similarity 86.1%; Pred. No. 1.1e-33; Nes 93; Conservative 8; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.8%; Score 486; DB 2; Length 123; 88.8%; Pred. No. 1.2e-33; rative 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross references: UNIPARC;UPI0000116151; EMBI
C;Superfamily: immunoglobulin V region; immunog
C;Reywords: heterotetramer; immunoglobulin
P;32-106/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: S40331
A; Status: preliminary; translation not shown
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig kappa chain V-J-C region - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-123 <KLB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig kappa chain - human
                                                                                                                                                                     A; Molecule type: mRNA
                                                                                                                                       A:Accession: S19674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95;
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
```

δ

ઠે

ï

9 75 ö

9

ö

9

유 ઠે 셤

```
C;Accession: $46372
R;Bensimon, C.; Chastagner, P.; Zouall, M.
EMBO 0.113, 2951-2962, 1994
A;Ttle: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene reas
A;Reference number: $46369; MUID:94313975; PMID:8039491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPARC:UP10000113F9C; GB:S77140; NID:g913352; PIDN:AAB34102.1; PID:
C;Ganetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CjAccession: 169017
R;Chin, L.T.; Duenas, M.; Levi, M.; Hinkula, J.; Wahren, B.; Borrebaeck, C.A.
Immunol. Lett. 44, 25-30, 1995
A;Title: Molecular characterization of a human anti-HIV 1 monoclonal antibody revealed a A;Reference number: 154563; MUID:95237884; PMID:7721339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anti-HIV1 envelope protein gpl20 V3 loop monoclonal antibody L chain V region - C;Species: Homo sapiens (man)
C;Species: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000
                                                                                              1 DIQLIQSPSSLSASVGDRVIITCRASQSVYNYVAWFQQKPGKAPKSLIYDASTLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 IRITQSPSSLSASTGDRVTITCRASQGISSYLAWYQQKPGKAPKLLIYAASTLQSGVPSR 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIQVTQSPSSLSASVGDRVTITCRASHDIGSYLAWYQQKPEKAPESLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                         IG light chain variable region (VJ) - human
C;Species: Homo sapiens (man)
C;Date: 07-May_1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
                                                              1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 IOMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
   Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 85.4%; Score 478; DB 2; Length 107; 1 Similarity 86.0%; Pred. No. 4.9e-33; 92; Conservative 6; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;COSB-references: UNIPARC:UP10000176CA4; EMBL:227173
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: Ig Vkappa
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>
9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 85.5%; Score 479; DB 2; Local Similarity 86.9%; Pred. No. 4.8e-33; les 93; Conservative 5; Mismatches 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; translated from GB/EMBL/DDBJ
   9; Mismatches
   90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Molecule type: mRNA
A; Regidues: 1-128 <BEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-107 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
   Matches
                                                                                                                                                                                                                                                                                                                                    RESULT 14
                                                                                                              셤
                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                              ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Map position: 2012-2012
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap main disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C; Complex: An immunoglobulin v region; immunoglobulin homology
C; Keywords: amyloid; heterotetramer; immunoglobulin homology
C; Keywords: amyloid; heterotetramer; immunoglobulin
F; 1-23/Region: Framework
F; 1-23/Region: complementarity-determining 1
F; 25-48/Region: complementarity-determining 2
F; 55-56/Region: complementarity-determining 2
F; 50-56/Region: complementarity-determining 3
F; 50-88/Region: complementarity-determining 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIOMIQSPSSLSASVGDRVIITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS 60
1 EIVLTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                           C;Species: Homo eaplens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig kappa chain V-I region (Ban) - numan
C;Species: Homo sapiens (man)
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 DIQLTQSPSFLSASIGDRVTITCRASQGINSYLAWYQQKPGKAPKLLIYVASTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                          C;Accession: $40334

Kiklein, R.; Jaenhaichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A;Title: Expressed human immunoglobulin chi genes and their hypermutation.

A;Reference number: $40312; MUID:94080891; PMID:8258341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ribwilet, F.E.; O'Connor, T.P.; Bengon, M.D.
Mol. Immunol. 23, 73-78, 1986
A,Title: POlymorphism in a kappa I primary (AL) amyloid protein (BAN)
A,Reference number: A01878; MUID:86174817; PMID:3083240
A,Accession: A01878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           °,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RPSGSGSGIDFTLTISSLQPEDFATYYCQQHNBYPLTFGQGTKVEIKR 108
                                                           61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNBYPLTFGQGTKVBIK 107
                                                                                                                    RPSGSGSGTDPTLTISSLQPEDPATYYCQQYSNYPLTPGGGTKVDIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 86.2%; Score 483; DB 2; Length 132; Best Local Similarity 85.2%; Pred. No. 2.3e-33; Matches 92; Conservative 7; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-132 «KLE»
A;Cross-references: UNIPARC:UPI0000176CA9; EMBL:X72444
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;37-111/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 1-108 <DWU>
A;Cross-references: UNIPROT:P04430; UNIPARC:UP1000012E150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85.9%; Score 481; DB 1;
83.3%; Pred. No. 2.8e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Accession: S40334
A, Status: preliminary; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98-107/Region: framework 4
23-88/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: GDB:136264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Accession: A01878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: GDB: IGKV1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genetics:
                                                                                                                                                                                                            RESULT 12
```

RESULT 13

셤 ò

8 გ £

human

ò

9

ö

61 RPSGSGSGTDFTLTISSLQPEDFATYYCQQYNSYPITFGQGTKVLIK 107

Search completed: April 13, 2006, 17:19:34 Job time : 23.1092 secs

# THIS PAGE IS BLANK

```
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
```

4	
mode	
36	
using	
search,	
protein	
٠	
protein	
ŏ	

		Bec
Seconda		updates/
April 13, 2006, 17:05:24 ; Search time 219.773 Seconds	(without alignments)	215.918 Million cell updates/sec
••		
17:05:24		
2006,		
ñ		
April		
Run on:		

US-10-727-737-2 Title: Perfect score:

1 DIQMTQSPSSLSASVGDRVT.....QQHNBYPLTFGQGTKVEIKR 108

Sequence:

2443163 segs, 439378781 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

2443163 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

Database

summaries

geneseqp2003as:\*geneseqp2003bs:\* geneseqp2001s:\*geneseqp2002s:\* geneseqp20048:\* A Geneseq 21:\* 1: geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp2005s:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Description		Aaw63529 Humanised		Adg38990 Humanised	_	_		Adf11669 anti-CD11	Human	Aay77752 Human lig	Aab30309 Human lig	Abul3786 Human lig	Human ]	Human	Aab46020 Human MUC	Aaw70622 Human con	Aay82345 Human con	Abp61191 Human ant		Human	Adp79572 Human kap	Human	Aea38745 Human VL	Aae28149 Human con
a	AAW62017	AAW63529	AAY82343	ADG38990	ADR03365	ADW38457	ADX80645	ADF11669	AAY29449	AAY77752	AAB30309	ABU13786	ABU59499	AAE39082	AAB46020	AAW70622	AAY82345	ABP61191	ADG38991	ADR03366	ADP79572	AAU74544	AEA38745	AAE28149
08	7	~	m	œ	œ	œ	σ	æ	~	m	m	9	9	7	4	7	٣	S	ω	æ	œ	S	σ	ß
* Query Match Length DB	108	108	108	108	108	108	108	214	109	109	109	109	109	109	240	108	108	108	108	108	108	109	109	110
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	97.6	97.6	97.6	97.6	97.6	97.6	91.4	90.4	90.4	90.4	90.4	90.4	90.4	90.4	90.4	90.4
Score	560	260	260	260	260	260	260	560	546.5	546.5	546.5	546.5	546.5	546.5	512	206	206	206	206	206	206	206	506	206
Result No.	, ,	8	m	4	S	v	7	80	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24

Aau09917 Light cha Abg75526 Humanised Ad123195 Human ant		Aabouvevo Consensus Aabels85 Human var Ade71454 Human ant Adi88008 Human var Adi19064 Variahle	Antibo Antibo Human Human	A9256737 AMINO aci Adm47073 Mouse ant Aab45993 Human MUC Ad036411 Intracell Aea41087 Germline
AAU09917 ABG75526 ADL23195	AAK40956 AAB45991 ADW04801 AAB62087	AAB60400 AAB61585 ADC71454 ADJ88008	ADN12034 ADP43328 ABJ18679 AAW27543 AAB46004	AAYS6737 ADM47073 AAB45993 ADO36411 AEA41087
4101	404	44000	00004	W L 4 8 0
127	2401.	1011	107 108 109 240	1224 1044 1088
2000	98999	88 88 88 8 9 9 8 8 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	8 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	88 88 1.1.88 88.88
505 505 505	2003 201 201 201 201	2011111	\$01 \$01 \$01	4 4 4 4 4 0 0 0 0 0 0 0 0 C C
25 26 27	300 78	9 9 9 7 7 7 9 7 9 7 9 7 9 9 9 9 9 9 9 9	4 U U U U U	144444 12644 12645

### ALIGNMENTS

Complementarity determining region; light chain variable region; humanised antibody; MFMA4F(ab)-8; anti-CD11a antibody; MFMA4 epitope; alpha subunit; lymphocyte function-associated antigen 1; LFA-1; immunoassay; in vivo imaging; diagnosis; CD11a-associated disease. Light chain variable region of humanised anti-CD11a antibody AAW62017 standard; peptide; 108 AA (first entry) 01-OCT-1998 AAW62017; AAW6201 

Homo sapiens Mus sp.

WO9823761-A1.

04-JUN-1998.

20-OCT-1997;

96US-00757205 27-NOV-1996;

97WO-US019041.

(GETH ) GENENTECH INC.

Presta LG; Jardieu PM,

WPI; 1998-322737/28.

New humanised anti-CD11a antibody - used in immunoassays for CD11a, and also to treat conditions such as immunological or inflammatory disease.

Claim 9; Page 48; 66pp; English.

The present sequence represents the light chain variable region of a humanised anti-CD11a antibody that binds specifically to the human CD11a fonain (WEM24 epitope). CD11a refers to the alpha subunit of lymphocyte function-associated antigen 1 (LFA-1) from any mammal. The humanised anti-CD1a antibodies are used to determine presence of CD11a in usual immunoassays or by in vivo imaging, particularly for diagnosis of CD11a-spsociated diseases (typically immune responses and inflammation such as postiasis, Crohn's disease, rheumatoid arthritis, transphant rejection,

ö

Gaps

ô

Length 108; 0; Indels

100.0%; Score 560; DB 2; 100.0%; Pred. No. 4.9e-33; 0; Mismatches

Best Local Simitarity Matches 108; Conservative

Query Match

6 9

1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS

음

```
This sequence represents the light chain of the humanised antibody MHM24, and was used to produce a mutant of the invention. The mutants are of a species-dependent antibody (Ab), and have an amino acid substitution in a variable region of the Ab, and binding affinity for an antigen (Ag) from a non-human mammal at least 10 times stronger than for the wild type Ab against the Ag. The mutant antibodies are particularly intended for against the Ag. The mutant antibodies are particularly intended for administration to a non-human mammal in preclinical studies (e.g. of infection, immunity, haematopolesis or transplantation). They can also be used diagnostically (to identify specific proteins) or therapeutically, c.g. where directed against CD11a (lymphocyte function-associated antigen inflammatory or autoimmune diseases, malignancies, transplant rejection, inflammatory or autoimmune diseases, malignancies, transplant rejection, conversion to the mutant form allows useful antibodies to be produced from antibodies which normally have affinity for non-human analogues of the Ag too low to be of any use
                                                                                       ö
                                                                                                                          9
                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibody mutant production, species-dependent antibody; malignancy; infection; haematopolesis; lymphocyte function-associated antigen-1; intercellular adhesion molecule-1; inflammatory disease; CDIIa; therapy; autoimmune disease; transplant rejection; tumour cell invasion; human immune deficiency virus infection; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mutants of species-dependent antibodies with affinity for non-human mammalian antigen - greater than for parent antibody, particularly used for pre-clinical trial(s) in rhesus monkey(s) of therapeutic antibodies directed against CD11a.
                                                                                                                                            1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                       Gape
                                                                                       .
0
                                                                                                                                                                                                               61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                    Length 108;
                                                                                     Indels
                                                   Score 560; DB 2;
Pred. No. 4.9e-33;
                                                                                       ö
                                  100.0%; Scc...
100.0%; Pred. No.....
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, Page 53; 71pp; English.
                                                                                                                                                                                                                                                                                                                  AAW63529 standard; protein; 108 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97WO-US020169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96US-00756150.
                                                                                                                                                                                                                                                                                                                                                                                                                        Humanised MHM24 light chain.
                                                                                                                                                                                                                                                                                                                                                                                     06-OCT-1998 (first entry)
                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Presta LG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-322726/28.
                                                                 Local Similarity
                  Sequence 108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9823746-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-JUN-1998
                                                                                   Matches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jardieu PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                    AAW63529;
                                                   Query Match
                                                                                                                                                                                                                                                                               RESULT 2
                                                                                                                                                                                                                                                                                              AAW63529
ž g
                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                         ò
                                                                                                                                                                                                                        셤
```

Sequence 108 AA;

```
The present invention describes a humanised anti-CD11a antibody (Ab) that binds specifically to the human CD11a I-domain. The Ab has anti-inflammatory, immunosuppressant, antitumour and antiviral activities. The Ab blocks lymphocyte function-associated with inflammatory hich is imvolved in leucocyte adhesion associated with inflammatory and immunological responses. The Ab are used: (1) optionally when coupled to a cytotoxin, to treat or prevent disorders mediated by lymphocyte function-associated antigen-1 (IrA-1; CD11a/CD18), e.g. psoriasis, inflammatory bowel disease, eczema, systemic lupus erythematosus, rhinitis, leukaemia, viral infections and many others, also for inhibiting graft rejection; (11) when labeled, to detect CD11a; (11) for inmunitis, leukaemiatory bowel disease, eczema, systemic lupus erythematosus, rhinitis, pertreatment; (14) for delivery of enzymes that convert producy to active anticodes as the murine antibodes from which they are derived. The murine antibody wink24 has ICSO 0.09 nM for preventing adhesion between Jurkat cells (expressing IFA-1) and normal epidermal converting the thully humanised version of MIMA-4 had ICSO 0.13 nM. The present sequence represents the light chain variable region of the humanised anti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New humanized anti-CD11a antibody, useful for treating or preventing e.g. inflammation and transplant rejection, contains human heavy variable region complementarity determining regions.
                                                                                                                                                                                                                                                                                                                   Humanised; anti-CD11a; antibody; anti-inflammatory; immunosuppressant; antitumour; antiviral; inflammation; immunological response; LFA-1; lymphocyte function-associated antigen-1; psoriasis; rhinitis; eczema; inflammatory bowel disease; systemic lupus erythematosus; leukaemia; viral infection; transplant rejection; graft rejection.
                                                                                                                                                                                                                                                                         Humanised anti-CD11a antibody light chain variable region SEQ ID NO:2.
                        61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVBIKR 108
  61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                 AAY82343 standard; protein; 108 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5; Fig 1; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-00974899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96US-0031971P.
                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jardieu PM, Presta LG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-282241/24.
                                                                                                                                                                                                                                    22-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JS6037454-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-MAR-2000
                                                                                                                                                                                          AAY82343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           жив вр
                                                                                                     RESULT 3
                                                                                                                        AAY82343
ઠે
```

```
27-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jardieu PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JUL-2004.
                                                                                                                                                                                                                                                                                                                                                           21-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VL; murine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapi
Chimeric.
                                                                                                                                                                                                                                                                                                                                ADR03365;
                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus sp.
                                                                                                                                         Matches
                                                                                                                                                                                                                                                                               RESULT 5
                                                                                                                                                                                                                                                                                            ADR03365
                                                                                                                                                                                                                                                                                                       888888888
                                                                                                                                                                 8
                                                                                                                                                                                        셤
                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                      g
                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CD) its antibody having specificity to human CD1s 1-domain or CD1s with a ket value of not more than 1x10-8 M, or concentration for 50 % inhibition (ICSO) (MM) value of not more than 1 m in mixed lymphocyte response assay or for preventing adhesion of Jurkat cells to normal human epidermal keratinocytes expressing intercellular adhesion molecule (ICAM) is the included are a kit comprising the antibody and instructions for use to detect the CD1s protein, an usel and instructions for antibody, a vector comprising the nucleic acid, a host cell so chat the antibody is expressed. The antibody by culturing the cell so that the antibody is expressed. The antibody by discussing the presence of CD1s protein and for treating lymphocyte function-associated antigen 1 mediated disorder such
                                                                                                                                                                                                                                                                                                                                         Mouse; CD11a; I-domain; monoclonal antibody; light chain variable region; VL; cluster of differentiation 11a; mixed lymphocyte response assay; Jurkat cell; epidermal keratinocyte; intercellular adhesion molecule; ICAM-1; lymphocyte function-associated antigen 1 mediated disorder; psoriasis; Crohn's disease; ulcerative colitis; dermatitis; aethma; rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis; diabetes mellitus; prodrug activating enzyme; humanised.
                                                                                                   9
                                                                                                                DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKILIYSGSTLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Humanized anti-CD11a antibody useful for treating lymphocyte function-
associated antigen mediated disorder e.g. psoriasis, Crohns disease,
ulcerative colitis, dermatitis, asthma, rheumatoid arthritis.
                                                                                                  DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention relates to a Humanised anti-cluster of differentiation
                                                                                                                                                                                                                                                                                                                    Humanised Mouse anti-CD11a antibody light chain variable region.
                                                                          ö
                                                                                                                                                     61 RPSGSGSGTDFTLTISSLQPEDFATYYCQQHNRYPLTFGQGTKVBIKR 108
                                                                                                                                                                  RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVBIKR 108
                                                 Length 108;
                                                                          0; Indels
                                                 ; Score 560; DB 3;
; Pred. No. 4.9e-33;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; SEQ ID NO 2; 43pp; English.
                                                                                                                                                                                                                                           ADG38990 standard; protein; 108 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96US-0031971P.
97US-00974899.
99US-00420745.
                                                  100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2001; 2001US-00795798.
                                                              100.08;
                                                                                                                                                                                                                                                                                            (first entry)
                                              Query Match
Best Local Similarity 100.
Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Presta LG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-051511/05.
                          Sequence 108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2003207336-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-OCT-1999;
                                                                                                                                                                                                                                                                                            26-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jardieu PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
 -CD11a Ab
                                                                                                                                                                                                                                                                     ADG38990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus sp.
                                                                                                                                                                                                                               ADG38990
                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                              8
                                                                                                                            윱
                                                                                                                                                     Š
                                                                                                                                                                            a
```

```
ö
as psoriasis, Crohn's disease, ulcerative colitis, dermatitis, asthma, rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis and diabetes mellitus. The antibody is useful when conjugated to a prodrug activating enzyme, or as an affinity purification agent. The present sequence is the light chain variable region (VL) of the humanised mouse anti-CD11a I domain monoclonal antibody MHM24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDlla antibody; human immunodeficiency virus infection; HIV infection; rhinovirus infection; inflammatory skin disease; psoriasis; inflammatory bowel disease; Crohn's disease; psoriasis; adult respiratory distress syndrome; allergic disease; eczema; asthma; autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus; SIE; diabetes mellitus; Reynaud's syndrome; immunological disease; tuberculosis; sarcoidosis; polymyositis; opp, CNS inflammatory disease; chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder; skin hypersensitivity disorder; poison ivy; poison oak; B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia; graft versus host disease; cancer; gene therapy; murine anti-human CDlla monoclonal antibody; MHM24; variable light chain; murine anti-human CDlla monoclonal antibody; MHM24; variable light chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antibody mutant of a species-dependent antibody, useful for treating and preventing infectious diseases, psoriasis, inflammatory bowel disease, allergic conditions, autoimmune diseases, or cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to an antibody mutant of a species-
dependent antibody with beneficial properties. The invention is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DIOMIQSPSSLSASVGDRVITICRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Humanised MHM24 F(ab)-8 antibody variable light chain protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLFGGGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 560; DB 8;
100.0%; Pred. No. 4.9e-33;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example; SEQ ID NO 2; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADR03365 standard; protein; 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-DEC-2003; 2003US-00727737.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96US-0031945P.
97US-00975329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
Les 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Presta LG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-552640/53.
                                                                                                                                                                                                                                                                                                Sequence 108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2004146507-A1
```

Sequence 108 AA;

ž g

```
for treating and preventing infectious diseases such as human immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin disease such as psoriasis, inflammatory bowel diseases such as Crohn's clisease such as psoriatis, adult respiratory distress syndrome, allergic diseases such as eczema and asthma, autoimmune diseases such as rheumatory systemic lupus errythematory distress syndrome, rheumatory course (Sist), diabetes mellitus, Reynaud's syndrome, immunological diseases such as tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary disease (COPD), CNS inflammatory disorder, skin hypersensitivity disorders such as poison ivy and poison oak, as cell malignancies such as chronic lymphocytic leukemia, and poison oak, as cell malignancies such as chronic lymphocytic leukemia and hairy cell leukaemia, graft versus host gisease and cancer. The invention is also useful in gene therapy. The present sequence is humanised murine anti-human CD11a monoclonal antibody (MFMV24) F(ab)-8 variable light chain protein. This sequence is used in the exemplification of the invention.
```

Sequence 108 AA;

```
ö
                                                                 9
                                                                                             9
                                                                                1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                  Gapa
                                  ö
                                                                                                                            61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                              RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
100.0%; Score 560; DB 8; Length 108; 100.0%; Pred. No. 4.9e-33; ive 0; Mismatches 0; Indels (
                Local Similarity 100.
Les 108; Conservative
                  Best Local Sim:
Matches 108;
 Query Match
                                                                ઠે
                                                                                            요
                                                                                                                           δ
                                                                                                                                                     g
```

ADW38457 standard; protein; 108 AA (first entry) 24-MAR-2005 ADW38457; 

```
CD11a light chain variable region #2
```

monoclonal antibody; CD11a; light-chain variable region; heavy-chain variable region.

Homo sapiens

CN1439651-A

03-SEP-2003

20-FEB-2002, 2002CN-00110866

20-FEB-2002; 2002CN-00110866.

(ZHON-) ZHONGXIN GUOJIAN PHARM CO LTD SHANGHAI

Wang H, Wang J;

WPI; 2004-169719/17.

Recombinant human CD11a monoclonal antibody and its preparation and medicinal composition.

Claim 1, Page 14; 16pp; Chinese.

The present invention relates to a recombinant monoclonal antibody for human CD11a has the amino acid sequence shown by SEQ ID No.1 or SEQ ID No.5 in light-chain variable region and the amino acid sequence shown by SEQ ID No.2 or SEQ ID No.6 in heavy-chain variable region. Its bloactivity and the expression in host cell are greatly increased. The DNA molecule for coding the antibody, its preparation process and the medicinal composition containing it are also disclosed. The present sequence represents a light chain variable region of human CD11a.

1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS 60

ò

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a method of purifying a protein which comprises a CH2/CH3 region by protein A affinity chromatography. The method involves reducing the temperature of a composition comprising the protein and one or more impurities subjected to protein A affinity chromatography to 3-20 degrees Celaius, where protein A leaching is reduced. Preferably the protein is antibody. The antibody and humanized VEGF antibody. Preferably, the antibody and humanized VEGF antibody. Preferably, the antibody binds HER2 antigen, where the antibody is grecifically a TMF receptor immunoadhesin. The methods are useful for purifying a protein, which comprises a CH2/CH3 region by protein A protein A affinity chromatography and for reducing leaching of protein A during protein A affinity chromatography. The current sequence represents the variable light chain amino acid sequence of CD11a.
                                                                                                                                                                                                                                                                                                                                                                                                                                Protein purification; leaching; protein A affinity chromatography; CD11a;
                                                                                                1 DIQMIQSPSSLSASVGDRVIITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS 60
                                                                           DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Purifying a protein, e.g. antibody or immunoadhesin, comprises reducin the temperature of a composition subjected to protein A affinity chromatography to 3-20 degrees C, where protein A leaching is reduced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                      Gapa
                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                       61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                  61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
 Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 108;
                                                                                                                                                                                                                                                                                                                                                                                           Humanized CD11a variable light chain amino acid sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; DB 9; Length 10
4.9e-33;
hes 0; Indels
                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₹,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oleary
 ; Score 560; DB 8;
; Pred. No. 4.9e-33;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 560; D. Best Local Similarity 100.0%; Pred. No. 4.9 Matches 108; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fahrner RL, Laverdiere A, Mcdonald PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 5; 27pp; English
                                                                                                                                                                                                                                                                               ADX80645 standard; protein; 108 AA.
Query Match
100.0%;
Best Local Similarity 100.0%;
Matches 108; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JUN-2004; 2004US-00877532.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-JUL-2003; 2003US-0490500P
                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2005-172327/18.
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2005038231-A1.
                                                                                                                                                                                                                                                                                                                                                         05-MAY-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-PEB-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                      ADX80645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibody
                                                                                                                                                                                                                                               RESULT
                                                                                                           셤
                                                                                                                                                  ò
```

61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108

```
AAY29449
                                                                               The invention relates to a method for purifying a target protein from a mixture containing a host cell protein. This method comprises subjecting the mixture to a non-affinity purification followed by high-performance tangential flow filtration (HPTFP) and isolating the protein in a purity containing less than 100 parts/million (ppm) of the host cell protein, where the method of the invention is useful for purification protein from a mixture containing a host cell protein, and is useful for protein grown a mixture containing a host cell protein, and is useful for incorporating the isolated protein into a pharmaceutical formulation. The proteins purified using the method of the invention are useful in a pharmaceutical respect, and are also useful in various diagnostic and therapeutic purposes. The method of the invention is efficient in purifying a target protein from a mixture containing a host cell protein, and may also be effectively performed at low cost. The current sequence represents the anti-CDII a rhumbh light chain amino acid sequence. This particular protein was used to demonstrate the method of the invention.
Purifying target protein from mixture containing host cell protein involves subjecting mixture to non-affinity purification, high-performance tangential flow filtration and isolating purified protein.
                                                                                                                                                                                                                                      Purifying; target protein; non-affinity purification;
high-performance tangential flow filtration; HPTFF; pharmaceutical;
diagnostic; therapeutic; antibody.
                                      RPSGSGSGTDFTLISSLQPEDFATYYCQQHNEYPLIFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 560; DB 8; Length 214; 100.0%; Pred. No. 8.9e-33; tive 0; Mismatches 0; Indels C
                                                                                                                                                                                                             anti-CD11a rhuMAb light chain amino acid sequence #SEQ ID 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Van Reis R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 3; 77pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lebreton B,
                                                                                                                                  ADF11669 standard; protein; 214 AA
                                                                                                                                                                                                                                                                                                                                                                         25-APR-2003; 2003WO-US013054.
                                                                                                                                                                                                                                                                                                                                                                                                   26-APR-2002; 2002US-0375953P.
                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Follman D,
                                                                                                                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-043096/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 214 AA;
                                                                                                                                                                                                                                                                                                                       WO2003102132-A2.
                                                                                                                                                                                      26-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pahner RL,
                                                                                                                                                                                                                                                                                                                                                 11-DEC-2003
                                                                                                                                                                                                                                                                                              Synthetic.
                                         61
                                                                                                                                                            ADP11669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                        RESULT
                                                                                                                                   ટ
```

```
New conjugates of nonproteinaceous polymers with antibody fragments, used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibody fragments covalently attached to one or more nonproteinaceous polymer molecules, where the apparent size of the conjugate is at least about 500 kDa. Conjugates of antibody fragments which blind the human interleukin (IL) 8 with a nonproteinaceous polymer can be used for treating inflammatory disorders e.g. acute lung injury, ischaemic treating inflammatory disorders e.g. acute lung injury, ischaemic treating e.g. inflammatory skin diseases including psoriasis and atopic dermatitis, systemic scleroderma and sclerosis, and asthmatic diseases. The conjugates can also be used as reagents in an animal model system for in vivo study of the biological functions of the antigen recognised by the conjugate. The present sequence represents the human light chain kappa-I consensus framework from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DIQMIQSPSSLSASVGDRVIITCRASKIISKYLAWYQQKPGKAPKLLIYYSGSTLESGVP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DIQMIQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLI-YSGSTLQSGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a novel conjugate having one or more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ġ
                                                                                                                                                                                                                              anti-IL-8 monoclonal antibody; interleukin 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zapata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 SRFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SRFSGSGSGTDFTLTISSLOPEDFATYYCQQHNEYPLTFGGGTKVEIKR 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 109;
                                                                                                                                                                                                                                                         diagnosis; inflammatory disorder; conjugate; immunoglobulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shahrokh Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97.6%; Score 546.5; DB 2
98.2%; Pred. No. 4.6e-32;
ive 1; Mismatches 0
                                                                                                                                                                    Human light chain kappa-I consensus framework.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Presta LG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for treating inflammatory disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Fig 29; 360pp; English.
AAY29449 standard; protein; 109 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leong SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-00012116.
98WO-US003337.
98US-00121952.
98US-00122513.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US001081.
                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Koumenis I,
                                                                                                                                                                                                                           Antibody; humanised;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-469134/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 109 AA;
                                                                                                                                                                                                                                                                                      fusion protein.
                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                               W09937779-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JAN-1999;
                                                                                                            05-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JAN-1998;
20-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-JUL-1998
                                                          AAY29449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hsei V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY77752
ID AAY7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
```

1;

AAY77752 standard; protein; 109 AA.

9 9

Gapa

ö

1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS

Conservative

Local Similarity

Best Local Simi Matches 108;

셤 ઠે

ð

61 RPSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVBIKR 108

```
99US-00234340.
                                                                                                                                                                                           Presta LG, Leong SR,
                                                                                                                                                                   (GETH ) GENENTECH INC
                                                                                                                                                                                                                 PI; 2000-686027/67.
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 109 AA;
                                      Homo sapiens
                                                                                                          20-FEB-1998;
                                                                                                                                            22-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US6468532-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-JAN-1999;
                                                                                                                                 21-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                            US6133426-A.
                                                                                    17-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABU13786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABU13786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ï
                                                                                Interleukin-8; IL-8; monoclonal antibody; MAb; anti-IL-8; 6G4.2.5VIIN35A; inflammatory disorder; adult respiratory distress syndrome; chimeric; affinity purification; 6G4.2.5.
                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an anti-interleukin-8 (IL-8) monoclonal antibody (MAb). The anti-IL-8 MAb comprises a sequence containing the CDRs (complementarity determining regions) of the humanized anti-IL-8 664.2.5VIN35A light chain, and amino acids 24-253 of the humanized anti-IL-8 664.2.5VIN35A heavy chain. The anti-IL-8 MAbs and fragments can be used in diagnosis, for affinity purification of IL-8 from recombinant cell culture or natural sources and for the treatment of inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Humanised antibody; anti-IL-8; interleukin-8; inflammation; septic shock;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorders e.g. adult respiratory distress syndrome. Nucleic acids encoding the anti-In-8 MAb can be associated in a vector with another gene encoding another protein or protein fragment to produce a fusion protein which can make isolation and/or purification of the protein an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid molecule encodes a polypeptide which is an anti-
interleukin-8 monoclonal antibody or antibody fragment useful for the
production of anti-interleukin-8 monoclonal antibodies or fragments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DIQMIQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLI-YSGSTLQSGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 SRPSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97.6%; Score 546.5; DB 3; Length 109; 98.2%; Pred. No. 4.6e-32; ive 1; Mismatches 0; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human light chain kappal consensus framework SEQ ID NO: 47.
                                                          Human light chain kl consensus framework
                                                                                                                                                                                                                                                                                      Gonzalez TN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                 Kample, Fig 29, 188pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB30309 standard; protein; 109
                                                                                                                                                                                                     98US-00027449.
                                                                                                                                                                                                                          97US-0038664P.
98US-0074330P.
                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 98.2
Matches 107, Conservative
                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                      Leong SR,
                                                                                                                                                                                                                                                                                                             WPI; 2000-181809/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sasier process
                                                                                                                                Homo sapiens
                                                                                                                                                                                                    20-FEB-1998;
                                                                                                                                                                                                                          21-FEB-1997;
22-JAN-1998;
                                  06-JUN-2000
                                                                                                                                                     US6025158-A
                                                                                                                                                                             15-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-FEB-2001
                                                                                                                                                                                                                                                                                     Presta LG,
            AAY77752;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB30309
1D AAB3
XX
AC AAB3
XX
DT 12-F
XX
XX
XX
XX
XX
XX
XX
XX
XX
ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
```

```
The present invention provides a number of humanised monoclonal anti-IL-8 antibodies which can be used in the diagnosis and treatment of inflammatory disorders, including adult respiratory distress syndrome, septite shock, multiple organ failure, bacterial pneumonia and inflammatory bowel disease. The present sequence comprises one of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIOMIQSPSSLSASVGDRVIIICRASKIISKYLAWYQQKPGKAPKLLI-YSGSILQSGVP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiinflammatory; respiratory; acute lung injury; polyethylene glycol; PEG; lung injury; adult respiratory distress syndrome; ARDS; asthma; inflammatory disease; psoriasis; solerosis; ischaemic try disease; inflammatory bowd disease; psoriasis; solerosis; ischaemic try disease; stroke; multiple sclerosis; meningitis; osteoarthritis; septic shock; autoimmune disease; rheumatoid arthritis; alcoholic hepatitis; cystic fibrosis; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Humanized anti-interleukin 8 monoclonal antibody variant useful for treating inflammatory disorders, such as adult respiratory distress syndrome, hypovolemic shock and ulcerative colitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibody, monoclonal antibody, 5.12.14; 6G4.2.5; interleukin-8; mAb;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SRFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGGGTKVEIKR 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 SRFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.6%; Score 546.5; DB 3; Length 109; 98.2%; Pred. No. 4.6e-32; ive 1; Mismatches 0; Indels 1.
adult respiratory distress syndrome; multiple organ failure; bacterial pneumonia; inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human light chain kappal consensus framework sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Col 161-162; 240pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gonzalez TN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABU13786 standard; protein; 109
                                                                                                                                                                                                                                                                                                                                                         98US-00026985.
                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0038664P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibodies of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 107; Conservative
```

ä

```
The invention relates to treating acute lung injury in a mammal, comprising administering to the mammal an effective amount of a conjugate comprising administering to the mammal an effective amount of a conjugate of a single antibody fragment covalently attached to 1 or 2 polyethylene glycol (PBG) molecules, where the antibody fragment is a F(ab') 2 comprising: (a) first chain that is either a light chain or a heavy chain opposite the first heavy chain; (c) a second chain that is either a heavy chain; and (d) a second opposite chain that is either a heavy chain; and (d) a second opposite chain that is either a heavy chain; where every EBG molecule is covalently attached to a first cysteine residue in the second cysteine residue in the first or second opposite chain, where the fab') 2 comprises an antigen binding site that binds to thuman interleukin-8 (IL-8), and where the apparent size of the conjugate chain, where the F(ab') 2 comprises an antigen binding sites may be derived from mutine monoclonal antibodies 5.12.14 or 664.2.5. The method is useful for treating lung injury, including adult respiratory distress syndrome (ARDS) in a mammal and inflammatory diseases (such as asthma, creperfusion disorders, stroke, multiple sclerosis, meningitis, osteoarthritis, septic shock, autoimmune disease (e.g. rheumatoid architis), alcoholic hepatitis, cystic fibrosis and many other diseases and disorders listed in the specification. The present sequence and disorders listed in the specification. The present sequence represents a human antibody sequences comparison with the represents a human antibody sequences.
                                                                                                                                                                                                                                                                                      Treating acute lung injury in mammal by administering to mammal a 500 kD conjugate comprising P(ab') 2 antibody fragment that binds to human interleukin-8, covalently attached to one or two polyethylene glycol
                                                                                                                                                                                              Zapata G;
                                                                                                                                                                                              Leong S, Presta L, Shahrokh Z,
                                                                                                                                                                                                                                                                                                                                                                                                                Example G; Fig 29; 259pp; English
                    98US-0074330P.
98US-0075467P.
98US-0094003P.
98US-0094013P.
                                                                                                                                                                                           Hsei V, Koumenis I,
                                                                                                                                           (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                           WPI; 2003-138230/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 109 AA;
                                             20-FEB-1998;
24-JUL-1998;
24-JUL-1998;
                      22-JAN-1998;
```

```
1 DIOMIQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYYSGSTLESGVP 60
                                             1; Gaps
                                                                                                                                                                         60 SRPSGSGSGTDFTLTISSLQPEDFATYYCQQHNBYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                 SRFSGSGGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 109
    6; Length 109;
                                             0; Indels
  97.6%; Score 546.5; DB 6; 98.2%; Pred. No. 4.6e-32; iive 1; Mismatches 0;
Query Match
Best Local Similarity 98.2
Matches 107; Conservative
                                                                                                                            셤
                                                                                                                                                                         ઠે
```

Human light chain kappal consensus framework. ABU59499 standard; protein; 109 AA. 22-APR-2003 (first entry) ABU59499; ABU59499 

RESULT 13

Interleukin-8; IL-8; humanised antibody; antibody; 5.12.14; 6G4.2.5; inflammatory disorder; psoriasis; atopic dermatitis; sclerosis; systemic scleroderms; inflammatory bowel disease; Crohn's disease; clohn's disease; clohn's disease; clohn's dischaemia; reperfusion; myocardial infarction; stroke; adult respiratory distress syndrome; rheumatoid arthritis; alcoholic hepatitis; acute lung injury; asthms; cerebral oedema; myocardial ischaemia, cranial trauma; asphyxia; Behcet's disease; dermatomyositis; polymyositis; multiple sclerosis; meningitis; encephalitis; uveitis; osteoarthritis; lupus nephritis; trauma; autoimmune disease; Slogren's syndrome; vasculitis; septicaemia; central nervous system inflammatory disorder; sepsis; sarcoidosis; inflammation of the lung; human.

US6458355-B1

01-OCT-2002

98US-00121952. 24-JUL-1998;

98US-0074330P. 22-JAN-1998; 20-FEB-1998; 

(GETH ) GENENTECH INC

Shahrokh Z, Presta L, Leong S, Koumenis I, Hsei V,

Treating inflammatory disorder in a mammal, involves administering a conjugate of polyethylene glycol and a single antibody fragment comprising antigen binding site that binds to human interleukin-8, to

Example 3G; Fig 29; 259pp; English.

The invention relates to treating an inflammatory disorder in a mammal, comprising administering to the mammal, an effective amount of a conjugate of a single antibody fragment (e.g. the heavy or light chains of the humanised mouse monoclonal antibodies 5.12.14 and 664.2.5, which also have their intramolecular disulphide bridges ablated by substitution also have their intramolecular disulphide bridges ablated by substitution of the humanised comprise an antigen binding site that binds to human interleukin-8 (IL-8), and the apparent size of the conjugate is at human interleukin-8 (IL-8), and the apparent size of the conjugate is at shock, in a mammal e.g. human. The method is useful for treating an inflammatory disorders including psoriasis, atopic dermatitis, systemic inflammatory disorders including psoriasis, atopic dermatitis, systemic scleroderma and sclerosis, responses associated with inflammatory bowel disease, ischaemic reperfusion disorders, myocardial ischaemic conditions, cerebral oedema secondary to stroke, cranial trauma, adult respiratory distress syndrome, acute-lung injury, esphoraes, datule associated with inflammatory bowel disease, dermatingitis, encephalitis, workits, osteoarthritis, lupus, dermating, autoimmune diseases such as rheumatoid arthritis, Slogren's syndrome, vasculitis, central nervous system inflammatory disorder, alcoholic hepatitis, accephalitis, uveitis, osteoarthritis, slogren's condition, batterial pneumonia, antigen-antibody complex alcoholic hepatitis, bacterial pneumonia, antigen-antibody complex alcoholic hepatitis, accephalitis, vorgan transplantation, inflammatory bowel disease such as ulceration, inflammatory bowel disease such as ulceration, of the lung, inflammatory bowel disease such as ulceration of human such as the to design the humanising mutations in the two mouse antibodies

Gaps 1; 97.6%; Score 546.5; DB 6; Length 109; 98.2%; Pred. No. 4.6e-32; ive 1; Mismatches 0; Indels 1; Matches 107; Conservative Best Local Similarity Sequence 109 AA; Query Match

ä

ω

```
60 SRFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR
                                                                                                                                                            AAB46020;
                                    61
                              셤
   53
                    The invention relates to novel conjugates comprising antibody fragments covalently attached to nomproteinaceous polymer molecules. The invention is useful for treating interleukin (IL) a mediated diseases or disorders such as inflammatory diseases, acute lung injury e.g. adult respiratory distress syndrome (ARDS), ischaemic reperfusion injury e.g. myocardial infarction, hypoolemic shock, inflammatory bowel disease e.g. ulcerative colitis, bacterial pneumonia and asthma. The invention is also useful as a reagent in an animal model system for in vivo study of the biological succious of the antigen recognised by the conjugate. The present sequence is human light chain kappal consensus framework protein. This sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                Interleukin-8 mediated disease; adult respiratory distress syndrome; IL; bacterial pneumonia; inflammatory bowel disease; hypoolemic shock; ARDS; ulcerative colitis; ischaemic reperfusion injury; myocardial infarction; acute lung injury; inflammatory disease; asthma; antibody; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel conjugates comprising antibody fragments covalently attached to nonproteinaceous polymer molecules, useful for treating inflammatory diseases, acute lung injury, ischemic reperfusion injury, pneumonia and
DIOMIQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLI-YSGSTLQSGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zapata
                                                                                         SRFSGSGSGTDFTLTISSLQPEDFATYYCQQHNBYPLTFGGGTKVBIKR 109
                                                                     SRFSGSGSGTDFTLTISSLOPEDFATYYCOOHNEYPLTFGOGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 7; Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shahrokh Z,
                                                                                                                                                                                                                                                                                                 Human light chain kappaI consensus framework protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 97.6%; Score 546.5; DB 7; Local Similarity 98.2%; Pred. No. 4.6e-32; es 107; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Presta L,
                                                                                                                                                                                               Z
                                                                                                                                                                                         AAE39082 standard; protein; 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example, Fig 29; 266pp, English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leong S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0074330P.
98US-0075467P.
98US-0094003P.
98US-0094013P.
99US-00234182.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-NOV-2000; 2000US-00726258
                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Heei V, Koumenis I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-605694/57
                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2003021790-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-JAN-1998;
                                                                                                                                                                                                                                                                18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-JUL-1998
                                                                       9
                                                                                                                                                                                                                              AAE39082;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    asthma
                                                                                                                                                        RESULT 14
                                                                                                                                                                       셤
                                                                     ઠે
                                                                                                  g
```

```
This invention describes a novel vaccine (V1) against conformation-
dependent antigens (CDA) comprising DNA (I) and/or an antibody, or
C dependent minimulogically imitates CDA, is new. (I) encodes a region
of an antidiotypic antibody (Ab2) or another peptide which: (a)
c binding molecule; and (b) immunologically minical the initial antigen. The
c pitcope is partially or completely conformation-dependent, and has an
immunogenic structure defined by a specific spatial conformation of amino
c pitcope is partially or completely conformation-dependent, and has an
immunogenic structure defined by a specific spatial conformation of amino
c conference and/or adjuvants. The products of the invention
c with a viral vector and/or adjuvants. The products of the invention
c vitostatic, virucidal, antibacterial and antiparasitic. The invention
c slso describes (1) a corresponding vaccine (V2) against antigens which
are not proteins or peptides, as defined above but which have epitopes
which show an immunogenic structure; (2) preparing (V1) and (V2); (3)
c which show an immunogenic structure; (2) preparing (V1) and (V2); (3)
c which show an immunogenic structure; (3) preparing (V1) and (V2); (3)
c which show an immunogenic structure; (4) MCI-conformation epitope
c which showing one of 13 approximately 60 residue amino acids sequences,
all fully defined in the specification; (4) MCI-conformation epitope
c minics having one of 16 9-17 residue amino acid sequences,
c the specification; (5) antidiotypic antibody fragments against the TF
c antigen having one of 24 approximately 200 residue amino acid sequences
c the specification; (5) The session amino acid sequences and secuence of the specification; (6) TF carbohydrate epitope minetics
c having one of 25 7-13 residue amino acid sequences and equences, and infectious diseases, e.g. caused by prions, viruses, bacteria
c and parasites. The vaccines are effective in cases where vaccination has
c previously not been possible
                                                                                                                                                                                                                                                                                                                           MUC1; human; vaccine; conformation-dependent antigen; antibody; cancer; antidiotypic antibody; cytostatic; virucidal; antibacterial; TF antigen; antiparasitic; infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaccines against conformation-dependent or non-peptide antigens, based on DNA encoding peptide which mimics the antigen, useful e.g. as antitumor
SRFSGSGSGTDFTLTISSLOPEDFATYYCQQHNEYPLTFGQGTKVEIKR 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 5-9; 36pp; German.
                                                                                                                                     AAB46020 standard; peptide; 240 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-MAY-2000; 2000WO-DE001809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99DE-01024405
99DE-01043016
                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                    Human MUC-1 scFv clone N1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Karsten U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-049937/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 240 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200073430-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-MAY-1999;
09-SEP-1999;
                                                                                                                                                                                                                                  23-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goletz S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vaccines.
```

DB 4; Length 240;

91.4%; Score 512;

Query Match

29 9

1;

Indels

Best Local

ò g

```
ö
                    Gaps
                  ;
0
Best Local Similarity 91.7%; Pred. No. 2.8e-29; Matches 99; Conservative 2; Mismatches 7; Indels
```

<u> වූ</u>

<sup>|</sup> Search completed: April 13, 2006, 17:13:39

## THIS PAGE IS BLANK